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(54) Title: NUCLEIC ACID ARRAYS

(57) Abstract

Arrays of polynucleotide spots and kits comprising the same, as well as methods for their preparation and use are provided. The subject arrays include a plurality of polynucleotide spots stably associated with the surface of a solid support. At least a portion of the polynucleotide spots comprises a polynucleotide probe composition that is made up of unique polynucleotides, where all of the unique polynucleotides of the array correspond to a common type of gene. Also provided are sets of a representational number of gene specific primers suitable for use in generating target nucleic acid for use with the subject arrays. The subject arrays find use in hybridization assays, particularly in assays for the identification of differential gene expression patterns among two or more different types of cells.

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NUCLEIC ACID ARRAYS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of application serial no. 08/859,998 filed on May 21, 1997 and application serial no. 09/053,375 filed on March 31, 1998, the disclosures of which are herein incorporated by reference.

INTRODUCTION

Technical Field

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The field of this invention is biopolymeric arrays.

Background of the Invention

"Biochips" or arrays of binding agents, such as oligonucleotides and peptides, have become an increasingly important tool in the biotechnology industry and related fields. These binding agent arrays, in which a plurality of binding agents are deposited onto a solid support surface in the form of an array or pattern, find use in a variety of applications, including drug screening, nucleic acid sequencing, mutation analysis, and the like. One important use of biochips is in the analysis of differential gene expression, where the expression of genes in different cells, normally a cell of interest and a control, is compared and any discrepancies in expression are identified. In such assays, the presence of discrepancies indicates a difference in the classes of genes expressed in the cells being compared.

In methods of differential gene expression, arrays find use by serving as a substrate to which is bound polynucleotide "probe" fragments. One then obtains "targets" from

analogous cells, tissues or organs of a healthy and diseased organism. The targets are then hybridized to the immobilized set of polynucleotide "probe" fragments. Differences between the resultant hybridization patterns are then detected and related to differences in gene expression in the two sources.

A variety of different array technologies have been developed in order to meet the growing need of the biotechnology industry, as evidenced by the extensive number of patents and references listed in the relevant literature section below.

Despite the wide variety of array technologies currently in preparation or available on the market, there is a continued need to identify new array devices to meet the needs of specific applications. Of particular interest would be the development of an array capable of providing high throughput analysis of differential gene expression.

Relevant Literature

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Patents and patent applications describing arrays of biopolymeric compounds and methods for their fabrication include: 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742 287; and EP 799 897.

Patents and patent application describing methods of using arrays in various applications include: 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280.

Other references of interest include: Atlas Human cDNA Expression Array I (April 1997) CLONTECHniques XII: 4-7; Lockhart et al., Nature Biotechnology (1996) 14: 1675-1680; Shena et al., Science (1995) 270: 467-470; Schena et al., Proc. Nat'l Acad. Sci. USA (1996)93:10614-10619; Shalon et al., Genome Res. (1996) 6: 639-645; Milosavljevic et al., Genome Res. (1996) 6:132-141; Nguyen et al., Genomics (1995)29: 207-216; Piétu et al., Genome Res. (1996) 6: 492-503; Zhao et al., Gene (1995) 166:207-213; Chalifour et al., Anal. Biochem. (1994) 216:299-304; Heller et al., Proc. Nat'l Acad. Sci. USA (1997) 94: 2150-2155; and Schena, M., BioAssays (1996) 18: 427-431.

SUMMARY OF THE INVENTION

Arrays of polynucleotide spots stably associated with the surface of a solid support and kits comprising the same, as well as methods for their preparation and use in hybridization assays, are provided. The subject arrays comprise a plurality of polynucleotide spots, wherein each different polynucleotide spot is made up of a polynucleotide probe composition and at least a portion of the polynucleotide probe compositions are made up of unique polynucleotides. The arrays are further characterized in that all of the unique polynucleotides on the array correspond to the same type of gene. The subject arrays find particular use in differential gene expression analysis. Also provided are sets of a representational number of gene specific primers useful in generating target nucleic acids for use with the subject arrays in hybridization assays.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 provides a representation of an array according to the subject invention.

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DEFINITIONS

The term "nucleic acid" as used herein means a polymer composed of nucleotides, e.g. deoxyribonucleotides or ribonucleotides.

The terms "ribonucleic acid" and "RNA" as used herein mean a polymer composed of ribonucleotides.

The terms "deoxyribonucleic acid" and "DNA" as used herein mean a polymer composed of deoxyribonucleotides.

The term "oligonucleotide" as used herein denotes single stranded nucleotide multimers of from about 10 to 100 nucleotides in length.

The term "polynucleotide" as used herein refers to single or double stranded polymer composed of nucleotide monomers of greater than about 120 nucleotides in length up to about 1000 nucleotides in length.

The term "array type" refers to the type of gene represented on the array by the unique polynucleotides, where the type of gene that is represented on the array is dependent on the intended purpose of the array, e.g. to monitor expression of key human genes, to monitor expression of known oncogenes, etc, i.e. the use for which the array is designed. As such, all of the unique polynucleotides on a given array correspond to the same type or

category or group of genes. Genes are considered to be of the same type if they share some common linking characteristics, such as: species of origin, e.g. human, mouse, rat, etc.; tissue or cell type of origin, e.g. muscle, neural, dermal, organ, etc.; disease state, e.g. cancer; functions, e.g. protein kinases, tumor supressors and the like, participation in the same normal biological process, e.g. apoptosis, signal transduction, cell cycle regulation, proliferation, differentiation etc.; and the like. For example, one array type that is provided below is a "cancer array" in which each of the "unique" polynucleotide probes correspond to a gene associated with a cancer disease state. Likewise, a "human array" may be an array of polynucleotides corresponding to unique tightly regulated human genes. Similarly, an "apoptosis array" may be an array type in which the polynucleotides correspond to unique genes associated with apoptosis.

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The "unique" polynucleotide sequences associated with each type of array of the present invention are sequences which are distinctive or different with respect to every other polynucleotide sequence on the array and correspond to the same type of gene, as defined above. For example, in a cancer array, each unique polynucleotide has a sequence that is not homologous to any other known cancer associated sequence. Moreover, each polynucleotide sequence on the array is statistically chosen to ensure that the probability of homology to any sequence of that type is very low. Morever, in the cancer array embodiment, all sequences are statistically chosen to insure that the probability of homology to any other sequence associated with cancer or of human origin is very low. An important feature of the individual polynucleotide probe compositions of the subject arrays is that they are only a fragment of the entire cDNA of the gene to which they correspond. In other words, for each gene represented on the array, the entire cDNA sequence the gene is not represented on the array. Instead, the sequence of only a portion or fragment of the entire cDNA is represented on the array by this unique polynucleotide.

The term "polynucleotide probe composition" refers to the nucleic acid composition that makes up each of the spots on the array. Thus, the term "polynucleotide probe composition" includes nucleic acid compositions of unique polynucleotides and control or calibrating polynucleotides (e.g. polynucleotides corresponding to housekeeping genes). The polynucleotide compositions are made up of single stranded polynucleotides (i.e. polynucleotides that are not hybridized to each other), where all of the polynucleotides in the probe composition may be identical to each other or there may be two different

polynucleotides (polynucleotides of different nucleotide sequence) in each probe composition, where the two different polynucleotides are complementary to each other.

The term "gene specific primer" means a polynucleotide of sufficient length to specifically hybridize to a distinct nucleic acid member of the sample, e.g. RNA or cDNA, where the length of the gene specific primers will usually be at least 8 nt, more usually at least 20 nt and may be as long as 25 nt or longer, but will usually not exceed 50 nt. The gene specific primers of the subject invention are sufficiently specific to hybridize to complementary template sequence during the generation of labeled nucleic acids under conditions sufficient for first strand cDNA synthesis, which conditions are known by those of skill in the art. The number of mismatches between the gene specific primer sequences and their complementary template sequences to which they hybridize during the generation of labeled nucleic acids in the subject methods will generally not exceed 20 %, usually will not exceed 10 % and more usually will not exceed 5 %, as determined using the FASTA program using default settings.

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DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Arrays of polynucleotide spots and methods for their preparation are provided. In the subject arrays, a plurality of polynucleotide spots is stably associated with the surface of a solid support, where at least a portion of the polynucleotide spots on the array are made up of unique polynucleotides and all of the unique polynucleotides of the array correspond to one particular type of gene, e.g. tightly regulated human genes, genes associated with a particular disease state, genes associated with cell cycle regulation, etc. The subject arrays find particular use in gene expression assays. Also provided are sets of a representational number of gene specific primers useful in generating target nucleic acids for use with the subject arrays. In further describing the subject invention, the arrays first will be described in general terms. Next, methods for their preparation are described. Following this, a description of representative specific array types falling within the scope of the invention will be provided. Finally, a review of representative applications in which the subject arrays may be employed will be provided, where this review includes a description of the sets of a representational number of gene specific primers according to the subject invention.

Before the subject invention is further described, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

ARRAYS OF THE SUBJECT INVENTION-GENERAL DESCRIPTION

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The arrays of the subject invention have a plurality of polynucleotide spots stably associated with a surface of a solid support. Each spot on the array comprises a polynucleotide sample, i.e. polynucleotide probe composition, of known identity, usually of known sequence, as described in greater detail below. The polynucleotide spots on the array may be any convenient shape, but will typically be circular, elliptoid, oval or some other analogously curved shape. The density of the spots on the solid surface is at least about 5/cm² and usually at least about 10/cm² but does not exceed about 1000/cm², and usually does not exceed about 300/cm². The spots may be arranged in any convenient pattern across or over the surface of the array, such as in rows and columns so as to form a grid, in a circular pattern, and the like, where generally the pattern of spots will be present in the form of a grid across the surface of the solid support. See Fig. 1.

In the subject arrays, the spots of the pattern are stably associated with the surface of a solid support, where the support may be a flexible or rigid solid support. By stably associated is meant that the polynucleotides of the spots maintain their position relative to the solid support under hybridization and washing conditions. As such, the polynucleotide members which make up the spots can be non-covalently or covalently stably associated

with the support surface. Examples of non-covalent association include non-specific adsorption, binding based on electrostatic (e.g. ion, ion pair interactions), hydrophobic interactions, hydrogen bonding interactions, specific binding through a specific binding pair member covalently attached to the support surface, and the like. Examples of covalent binding include covalent bonds formed between the spot polynucleotides and a functional group present on the surface of the rigid support, e.g. -OH, where the functional group may be naturally occurring or present as a member of an introduced linking group, as described in greater detail below.

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As mentioned above, the array is present on either a flexible or rigid substrate. By flexible is meant that the support is capable of being bent, folded or similarly manipulated without breakage. Examples of solid materials which are flexible solid supports with respect to the present invention include membranes, e.g. nylon, flexible plastic films, and the like. By rigid is meant that the support is solid and does not readily bend, i.e. the support is not flexible. As such, the rigid substrates of the subject arrays are sufficient to provide physical support and structure to the polymeric targets present thereon under the assay conditions in which the array is employed, particularly under high throughput handling conditions. Furthermore, when the rigid supports of the subject invention are bent, they are prone to breakage.

The solid supports upon which the subject patterns of spots are presented in the subject arrays may take a variety of configurations ranging from simple to complex, depending on the intended use of the array. Thus, the substrate could have an overall slide or plate configuration, such as a rectangular or disc configuration. In many embodiments, the substrate will have a rectangular cross-sectional shape, having a length of from about 10 mm to 200 mm, usually from about 40 to 150 mm and more usually from about 75 to 125 mm and a width of from about 10 mm to 200 mm, usually from about 20 mm to 120 mm and more usually from about 25 to 80 mm, and a thickness of from about 0.01 mm to 5.0 mm, usually from about 0.1 mm to 2 mm and more usually from about 0.2 to 1 mm.

The substrates of the subject arrays may be fabricated from a variety of materials. The materials from which the substrate is fabricated should ideally exhibit a low level of non-specific binding during hybridization events. In many situations, it will also be preferable to employ a material that is transparent to visible and/or UV light. For flexible substrates, materials of interest include: nylon, both modified and unmodified, nitrocellulose,

polypropylene, and the like, where a nylon membrane, as well as derivatives thereof, is of particular interest in this embodiment. For rigid substrates, specific materials of interest include: glass; plastics, e.g. polytetrafluoroethylene, polypropylene, polystyrene, polycarbonate, and blends thereof, and the like; metals, e.g. gold, platinum, and the like; etc.

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The substrates of the subject arrays comprise at least one surface on which the pattern of spots is present, where the surface may be smooth or substantially planar, or have irregularities, such as depressions or elevations. The surface on which the pattern of spots is present may be modified with one or more different layers of compounds that serve to modify the properties of the surface in a desirable manner. Such modification layers, when present, will generally range in thickness from a monomolecular thickness to about 1 mm, usually from a monomolecular thickness to about 0.1 mm and more usually from a monomolecular thickness to about 0.001 mm. Modification layers of interest include: inorganic and organic layers such as metals, metal oxides, polymers, small organic molecules and the like. Polymeric layers of interest include layers of: peptides, proteins, polynucleic acids or mimetics thereof, e.g. peptide nucleic acids and the like; polysaccharides, phospholipids, polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneamines, polyarylene sulfides, polysiloxanes, polyimides, polyacetates, and the like, where the polymers may be hetero- or homopolymeric, and may or may not have separate functional moieties attached thereto, e.g. conjugated.

The total number of spots on the substrate will vary depending on the number of different polynucleotide probes one wishes to display on the surface, as well as the number of control spots, calibrating spots and the like, as may be desired depending on the particular application in which the subject arrays are to be employed. Generally, the pattern present on the surface of the array will comprise at least about 10 distinct spots, usually at least about 20 distinct spots, and more usually at least about 50 distinct spots, where the number of spots may be as high as 10,000 or higher, but will usually not exceed about 5,000 distinct spots, and more usually will not exceed about 3,000 distinct spots. In many embodiments, it is preferable to have each distinct probe composition presented in duplicate, i.e. so that there are two spots for each distinct polynucleotide probe composition of the array. In certain embodiments, the number of spots will range from about 200 to 600.

The amount of polynucleotide present in each spot will be sufficient to provide for adequate hybridization and detection of target nucleic acid during the assay in which the

array is employed. Generally, the amount of polynucleotide in each spot will be at least about 0.1 ng, usually at least about 0.5 ng and more usually at least about 1 ng, where the amount may be as high as 1000 ng or higher, but will usually not exceed about 20 ng and more usually will not exceed about 10 ng. The copy number of each polynucleotide in a spot will be sufficient to provide enough hybridization sites for target molecule to yield a detectable signal, and will generally range from about 0.01 fmol to 50 fmol, usually from about 0.05 fmol to 20 fmol and more usually from about 0.1 fmol to 5 fmol. Where the spot has an overall circular dimension, the diameter of the spot will generally range from about 10 to 5,000 μ m, usually from about 20 to 2,000 μ m and more usually from about 50 to 1000 μ m.

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A critical feature of the subject arrays is that at least a portion, usually the majority, of the polynucleotide spots on the array are made up of polynucleotide probes that all correspond to the same kind or kind of gene, i.e. genes that all share some common characteristic or can be grouped together based on some common feature, such as species of origin, tissue or cell of origin, functional role, disease association, etc. Other spots which may be present in the pattern include spots comprising genomic DNA, housekeeping genes, negative and positive control genes, and the like. These latter types of spots comprise polynucleotides that are not "unique" as that term is defined and used herein, i.e. they are "common." In other words, they are calibrating or control genes whose function is not to tell whether a particular "key" gene of interest is expressed, but rather to provide other useful information, such as background or basal level of expression, and the like. The percentage of spots which are made of unique polynucleotides that correspond to the same type of gene is generally at least about 30 number %, and usually at least about 60 number % and more usually at least about 80 number %. Therefore, the arrays of the subject invention will be of a specific array type, where representative array types include: human arrays, mouse arrays, cancer arrays, apoptosis arrays, human stress arrays, oncogene and tumor suppressor arrays, cell-cell interaction arrays, cytokine and cytokine receptor arrays, rat arrays, blood arrays, mouse stress arrays, neuroarrays, and the like, where some of these representative arrays are described in greater detail below.

With respect to the polynucleotide probes that correspond to a particular type or kind of gene, type or kind can refer to a plurality of different characterizing features, where such features include: species specific genes, where specific species of interest include eukaryotic

species, such as mice, rats, rabbits, pigs, primates, humans, etc.; function specific genes, where such genes include oncogenes, apoptosis genes, cytokines, receptors, protein kinases, etc.; genes specific for or involved in a particular biological process, such as apoptosis, differentiation, cell cycle regulation, cancer, aging, proliferation, etc.; location specific genes, where locations include organ, such as heart, liver, prostate, lung etc., tissue, such as nerve, muscle, connective, etc., cellular, such as axonal, lymphocytic, etc., or subcellular locations, e.g. nucleus, endoplasmic reticulum, Golgi complex, endosome, lyosome, peroxisome, mitochondria, cytoplasm, cytoskeleton, plasma membrane, extracellular space; specific genes that change expression level over time, e.g. genes that are expressed at different levels during the progression of a disease condition, such as prostate genes which are induced or repressed during the progression of prostate cancer.

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The average length of the polynucleotides on the array is chosen to be of sufficient length to provide a strong and reproducible signal, as well as tight and robust hybridization. As such, the average length of the polynucleotides of the array will typically range from about 120 to 1000 nt and usually from about 120 to 800 nt, where in many embodiments, the average length ranges from about 200 to 700 nt, and usually 200 to 600 nt. The length of each polynucleotide on the array is less than the length of the mRNA to which it corresponds. As such, the polynucleotide represents only a fraction of the full length cDNA to which it corresponds.

As mentioned above, the subject arrays typically comprise one or more additional spots of polynucleotides which do not correspond to the array type, i.e. the type or kind of gene represented on the array. In other words, the array may comprise one or more spots that are made of non "unique" polynucleotides, i.e common polynucleotides. For example, spots comprising genomic DNA may be provided in the array, where such spots may serve as orientation marks. Spots comprising plasmid and bacteriophage genes, genes from the same or another species which are not expressed and do not cross hybridize with the cDNA target, and the like, may be present and serve as negative controls. In addition, spots comprising housekeeping genes and other control genes from the same or another species may be present, which spots serve in the normalization of mRNA abundance and standardization of hybridization signal intensity in the sample assayed with the array.

Polynucleotide Probes of the Arrays

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Each spot of the pattern present on the surface of the substrate is made up of a unique polynucleotide probe composition. By "polynucleotide probe composition" is meant a collection or population of single stranded polynucleotides capable of participating in a hybridization event under appropriate hybridization conditions, where each of the individual polynucleotides may be the same -- have the same nucleotide sequence-- or different sequences, for example the probe composition may consist of 2 different single stranded polynucleotides that are complementary to each other (i.e. the two different polynucleotides in the spot are complementary but physically separated so as to be single stranded, i.e. not hybridized to each other). In many embodiments, the probe compositions will comprise two complementary, single stranded polynucleotides.

In those polynucleotide probe compositions having unique polynucleotides, the sequence of the polynucleotides are chosen in view of the type and the intended use of the array on which they are present. The unique polynucleotides are chosen so that each distinct unique polynucleotide does not cross-hybridize with any other distinct unique polynucleotide on the array, i.e. the polynucleotide of any other polynucleotide probe composition that corresponds to a different gene falling within the broad category or type of genes represented on the array. As such, the nucleotide sequence of each unique polynucleotide of a probe composition will have less than 90% homology, usually less than 85 % homology, and more usually less than 80% homology with any other different polynucleotide of a probe composition of the array, where homology is determined by sequence analysis comparison using the FASTA program using default settings. The sequence of unique polynucleotides in the probe compositions are not conserved sequences found in a number of different genes (at least two), where a conserved sequence is defined as a stretch of from about 40 to 200 nucleotides which have at least about 90% sequence identity, where sequence identity is measured as above. The polynucleotide will generally be a deoxyribonucleic acid having a length of from about 120 to 1000, usually from 120 to 700 nt, and more usually 200 to 600 nt. The polynucleotide will not cross-hybridize with any other polynucleotide on the array under standard hybridization conditions. Again, the length of the polynucleotide will be shorter than the mRNA to which it corresponds.

Array Preparation

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The subject arrays can be prepared using any convenient means. One means of preparing the subject arrays is to first synthesize the polynucleotides for each spot and then deposit the polynucleotides as a spot on the support surface. The polynucleotides may be prepared using any convenient methodology, such as automated solid phase synthesis protocols, preparative PCR and like, where preparative PCR or enzymatic synthesis is preferred in view of the length and the large number of polynucleotides that must be generated for each array.

For preparative PCR, primers flanking either side of the portion of the gene of interest will be employed to produce amplified copy numbers of the portion of interest. Methods of performing preparative PCR are well known in the art, as summarized in PCR, Essential Techniques (Ed. J.F. Burke, John Wiley & Sons)(1996). Alternatively, if a gene fragment of interest is cloned into a vector, vector primers can be used to amplify the gene fragment of interest to produce the polynucleotide.

In determining the portion of the gene to be amplified and subsequently placed on the array, regions of the gene having a sequence unique to that gene should preferably be amplified. Different methods may be employed to choose the specific region of the gene to be amplified. Thus, one can use a random approach based on availability of a gene of interest. However, instead of using a random approach which is based on availability of a gene of interest, a rational design approach may also be employed to choose the optimal sequence for the hybridization array. Preferably, the region of the gene that is selected and amplified is chosen based on the following criteria. First, the sequence that is chosen should yield a polynucleotide that does not cross-hybridize with any other polynucleotide that is present on the array. Second, the sequence should be chosen such that the polynucleotide has a low probability of cross-hybridizing with a polynucleotide having a nucleotide sequence found in any other gene, whether or not the gene is to be represented on the array from the same species of origin, e.g. for a human array, the sequence will not be homologous to any other human genes. As such, sequences that are avoided include those found in: highly expressed gene products, structural RNAs, repeated sequences found in the sample to be tested with the array and sequences found in vectors. A further consideration is to select sequences which provide for minimal or no secondary structure, structure which allows for

optimal hybridization but low non-specific binding, equal or similar thermal stabilities, and optimal hybridization characteristics.

The prepared polynucleotides may be spotted on the support using any convenient methodology, including manual techniques, e.g. by micro pipette, ink jet, pins, etc., and automated protocols. Of particular interest is the use of an automated spotting device, such as the Beckman Biomek 2000 (Beckman Instruments). As mentioned above, the polynucleotide probe compositions that are spotted onto the array surface are made up of single stranded polynucleotides, where all the polynucleotides may be identical to each other or a population of complementary polynucleotides may be present in each spot.

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SPECIFIC ARRAY TYPES OF THE SUBJECT INVENTION

A variety of specific array types are also provided by the subject invention. As discussed above, array type refers to the nature of the polynucleotide probes present on the array and the types of genes to which the probes correspond. These array types include: human array; mouse array; cancer array, apoptosis array, human stress array, oncogene and tumor suppressor arrray, cell-cell interaction array, and cytokine and cytokine receptor array, as well as other types of arrays, e.g. rat array, rat stress array, blood array, mouse stress array, and nueroarray. Each of these arrays is described separately below.

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Human Array

One specific array type provided by the subject invention is the human array. In the human array of the subject invention, the majority of the spots on the array have a polynucleotide sequence corresponding to a human gene of interest. As such, all of the unique polynucleotide probes on the array correspond to human genes. The human genes represented on the human array are typically those genes that have been identified by those of skill in the art as key genes. By "key" is meant that the genes are relevant and related to the purpose of the array, e.g. the identification of difference in the expression profiles of different cell or tissue types, where the key genes are generally functionally important to the cell. In many embodiments, the genes represented on the human array are tightly regulated human genes. The term "tightly regulated gene" is used herein in accordance with its art accepted definition and use. As such, by tightly regulated human gene is meant a gene which

is not "leaky," as opposed to housekeeping genes which are generally expressed at similar levels in different cells and different tissues, i.e. a gene which is inducible such that in response to a specific inducing signal the gene turns "on" and when this signal is removed, the gene turns "off."

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In certain embodiments of the human array, human genes that may be represented on the subject arrays include: (a) oncogenes & tumor suppressors; (b) cell cycle regulators; (c) stress response proteins; (d) ion channel & transport proteins; (e) intracellular signal transduction modulators and effectors; (f) apoptosis-related proteins; (g) DNA synthesis, repair and recombination proteins; (h) transcription factors & general DNA binding proteins; (i) growth factor & chemokine receptors; (j) interleukin & interferon receptors; (k) hormone receptors; (l) neurotransmitter receptors; (m) cell surface antigens & cell adhesion proteins; (n) growth factors, cytokines and chemokines; (o) interleukins & interferons; (p) hormones; (q) extracellular matrix proteins; (r) cytoskeleton & motility proteins; (s) RNA processing & turnover proteins; (t) post-translational modification, trafficking & targeting proteins; (u) protein turnover; and (v) metabolic pathway proteins.

In view of the length of the polynucleotides of the probe compositions of the spots, each polynucleotide of a probe composition typically has a nucleotide sequence of only a portion of the human gene. Specific sequences to which the polynucleotide sequence may correspond include those identified in Table 1 below, where by "correspond" is meant that the polynucleotide could have the same sequence as specified or a sequence complementary to the specified sequence. Whether the polynucleotide sequence is the same as a portion of the sense strand of the gene to which is corresponds or complementary thereto is based primarily on the nature of the target which the array is to be used, e.g. if the target is first strand cDNA, the polynucleotide will have a sequence found in the anti-sense DNA strand of the gene to which it corresponds.

Of particular interest is a human array of the subject invention as shown in Fig. 1. In the array, each spot on the array comprises a known polynucleotide, as specified in Table 1, where the array comprises spots which: (a) correspond to 588 different tightly regulated human genes; (b) comprise plasmid and bacteriophage polynucleotides; (c) comprise polynucleotides corresponding to housekeeping genes; and (d) genomic DNA. Each of the different types of polynucleotide spots are positioned at a known location on the membrane surface.

TABLE 1

			Docition
Array Coordinate	GeneBank #	Gene Name	LOSIGOI LOS CONT
E2I	M29696	interleukin-7 receptor (IL-7)	1410-1625
F5i	X01992, M29383	HUIFN-gamma interferon	391-586
F5i	J04156	interleukin 7 (IL-7)	174-447
A1a	V00568	c-myc oncogene	1372-1594
F2m	X01057, X01058, X01402	interleukin-2 receptor	1990-2247
F5k	- 1	interleukin-2 (IL-2)	181-436
F1a	M29366	epidermal growth factor receptor (ERBB3)	3886-4139
C1a	X04434, M24599	insulin-like growth factor I receptor	3414-3904
F13	M29645	insulin-like growth factor II	436-618
Clb	L09210	homo sapiens inducible nitric oxide synthase	3503-3856
F4f	M64752	glutamate receptor subunit (GLUH1)	2232-2567
A1h	X03663	c-fms proto-oncogene	2568-2880
213	M32315	tumor necrosis factor receptor	3359-3543
C1d	Z12020	p53-associated gene	920-1232
F1b	X02811	platelet-derived growth factor B chain	1663-2125
B1d	X01060	transferrin receptor	4382-4770
F51	X02851	interleukin-1 precursor (PRE IL-1)	1107-1473
F5m	K02770	monocyte interleukin 1 (IL-1)	917-1208
F5n	M14743	interleukin 3 (IL-3)	390-608
F6a	M13982	interleukin 4 (IL-4)	216-459
F6b	X04602	interleukin BSF-2 (B-cell differentiation factor)	130-555
C1e	X01394	tumor necrosis factor	607-879
C1f	D12614	lymphotoxin (TNF-BETA)	305-499
F5c	M12807	T-cell surface glycoprotein T4	947-1140
E2n	M20566, X12830	interleukin 6 receptor	2359-2823
F6c	X04688	T-cell replacing factor (interleukin-5)	35-279
F6d	M28622	interferon beta-1 (IFN-beta-1)	345-730
F1c	M11220	granulocyte-macrophage colony stimulating factor	121-621
F1d	K03222	transforming growth factor-alpha	338-595
F6e	J00209	leukocyte interferon (IFN-alpha) alpha-C	89-430
F1e	X02812, J05114	transforming growth factor-beta (TGF-beta)	2398-2575
11	X03438	granulocyte colony-stimulating factor (G-CSF)	901-1232
D1a	M58603	nuclear factor kappa-B DNA binding subunit	2544-3019
A1c	M15024	nucleotide sequence of the c-myb cDNA clone lambda-LMC8	1981-2176
C10	M14694	p53 cellular tumor antigen	690-964
F10	M19154, M22045, M22046	transforming growth factor beta-2	1538-1878
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TABLE 1 (CONT)

		1.		ſ
Array Coordinate	\neg	Gene Name	Position	
F1h	X04571	kidney epidermal growth factor (EGF) precursor	4164-4434	
E3a	J03171	interferon alpha receptor (HUIFN-ALPHA-REC)	2562-2740	
F6f	M57627	interleukin 10 (IL10)	442-648	
E3b	M26062	interleukin 2 receptor beta chain (P70-75)	3399-3748	
E3c	M74782	interleukin 3 receptor (HIL-3RA)	651-1116	
E3d	X52425	interleukin 4 receptor	2641-2974	
E3e	M75914	interleukin 5 receptor alpha	555-959	
E3f	X77722	interferon alpha/beta receptor	553-1012	
臣	HG1621	cytokine humig	2021-2246	
E4g	HG1160, M37981	cholinergic receptor nicotinic alfa polipeptide 3	934-1250	
E3g	HG1252, D11086	interleukin 2 receptor gamma polipeptide	674-1006	
E4b	HG1334, M20132, J03180	androgen receptor	1879-2146	
E16	HG135, M73238	ciliary neurotropic factor receptor	610-849	
C1h	HG1410, X68486	adenosine receptor	1281-1494	
E3h	HG1757, J03143	interferon gamma receptor	610-824	
E1c	HG2246, M60459	erythropoietin receptor	1423-1740	
C1i	S56143	A1 adenosine receptor-adenylate cyclase inhibitor	508-921	
B1e	HG3354, Z30425	orphan hormone nuclear receptor	817-1147	
C1j	HG3381, X76981	adenosine receptor A3	1043-1452	
E4c	L00587	calcitonin receptor	885-1270	
B1f	HG74, M62424	coagulating factor II receptor	2297-2697	
A1e	HG886, L07594	transforming growth factor beta receptor III 300 kDa	3358-3592	
E3i	HG216, M84747	interleukin 9 receptor	289-528	
E3j	HG4080, U00672	interleukin 10 receptor	2448-2803	
E1d	HG423, M14764	nerve growth factor receptor	2762-3242	
E5d	HG1023	Vitronectin receptor alpha subunit	2442-2473	
D1b	HG125	GATA-binding protein 2	1126-1363	
D1c	HG1377	CCAAT-box DNA-binding protein Hap2 homolog	958-1272	
C1k	HG1458	retinoic acid receptor epsilon	1315-1633	
A1f	HG1470, X13293	B-myb	1873-2272	
B1g	HG1551	tyrosine kinase receptor tie	3114-3536	
C1I	HG1601	tyrosine kinase receptor FLT4 class III	4236-4402	
D1d	HG1603	helix-loop-helix protein 1R21	858-560	
F1j	HG1650	thrombomodulin	1262-1605	
D1e	HG1697	basic transcription element-binding protein 2	572-976	
D1f	HG1963	basic transcription factor 62 kDa subunit	1449-1831	

TABLE I (CONT)

Array Coordinate	GeneBank #	Gene Name	Position
Alfay coolulisate	HG1972	helix-loop-helix protein Id-2	111-382
מא	HG2094	andiotensin II type 1a receptor alt splice 1	1855-2030
E40	HG209	tyrosine kinase receptor HEK	2826-3144
110	HG9158	DNA-binding protein SMBP2	1587-1911
1 2	HG244	global transcription activator	1621-1886
- T	HG2480	FMLP-related receptor I	349-657
. B.1:	HG2490	transmembrane receptor ror1	3044-3302
<u>.</u>	HG2722	tyrosine kinase KDR receptor	2686-3053
D1;	HG277	DNA-binding protein ICS	1253-1475
A10	HG2811	thyroid hormone triiodothyronine receptor c-erbA ear-1	1676-2100
D1k	HG2869	CACCC-box DNA-binding protein	1686-2063
R1k	HG2892, X75208	tyrosine kinase receptor	2551-2820
		DNA-binding protein TAX	359-765
E	HG3314	tyrosine kinase receptor TKT	2621-2989
- E	1 25124	prostaglandin E2 receptor	1818-2029
a t	HG1187	epidermal growth factor receptor	3410-3757
TT-1	HG1662	platelet-activating factor receptor	1103-1398
2.00	HG1830	tyrosine phosphatase receptor eph alt splice 1	2607-3053
D1m	HG3428	DNA-binding protein/plasminogen activator inhibitor-1 regulator	1304-1736
E.3.	HG3446, A09781	interferon gamma receptor	66-317
D1n	HG3463	DNA-binding protein CN sterol regulating	96-341
A1h	HG3509	v-erbA related ear-2 protein	882-1057
41	HG3510	v-erbA related ear-3 protein	1449-1700
029	HG3548	CCAAT displacement protein cut homolog alt splice 1	2000-2400
D2h	HG3748	basic transcription factor 44 kDa subunit	606-843
02c	HG3957	DNA-binding protein APRF	1545-1575
D2d	HG4002	estrogen receptor hSNF2b	2415-2682
B2a	HG4196	urokinase-type plasminogen activator receptor	749-1043
A1i	HG4269	Ets-like gene	710-1064
R2h	HG4279	tyrosine kinase TRK-B receptor	1006-1384
D2e	HG4574	DNA-binding protein NFX1 cysteine-rich specific	2003-2311
A5h	HG4579	DP2 dimerization partner of E2F	1603-1838
F1	HG563	glia maturation factor beta	203-434
D2f	HG753	DNA-binding protein TAXREB67	1059-1495
D20	HG859, L05515	cAMP-responsive element-binding protein	807-1120
A1k		tyrosine kinase EGF receptor Her4	3570-3965

TABLE 1 (CONT)

			Docition
Array Coordinate	-	Gene Name	TOSKIDII
B2c	HG918	tyrosine phosphatase receptor gamma polypeptide	3023-3930
אכם	HG970	DNA-binding protein PO-GA	3196-3413
125	HG99. M64673	CCAAT enhancer-binding protein beta	294-572
D2 A1	.104111	c-jun proto-oncogene (jun) clone HCJ-1	2207-2583
F3	M27492	interleukin 1 receptor	3847-4288
E10	M33294	tumor necrosis factor receptor	1570-1817
E13	M37435	macrophage-specific colony-stimulating factor (CSF-1)	2277-2413
A1m	YOO285	insulin-like growth factor II receptor	1394-1831
Δ10	HG404	tyrosine kinase receptor HER2	2556-2722
Rod	D10923	HM74	1357-1826
B2e	D10924	HW89	351-808
970	D10025	HM145	1353-1832
D21	D10050	henatocyte growth factor activator precursor	1487-1845
100	D14012	henatoma-derived growth factor	359-625
רבמ	D30751	bone morphogenetic protein 4	943-1321
F 20	103358	FER tyrosine kinase	2384-2688
DZG L'OS	104130	activation (Act-2)	236-592
בטק	105081	endothelin ET3	1428-1685
003	K03515	neuroleukin	1368-1656
27.4	1.00015	TEK tyrosine kinase receptor	3243-3586
750	1.06622	endothelin receptor EDNRA	870-1080
D 4	1 06693	endothelin receptor EDNRB	497-814
E E	1.06801	interleukin IL-13	285-743
5	1 07414	CD40 ligand	863-1277
C2a	1 08096	CD27 ligand	233-627
Fam	1.08187	cytokine receptor (EB13)	627-1019
F2f	12260	glial growth factor 2 (recombinant)	1069-1452
F2n	L12261	glial growth factor (recombinant)	762-1041
E L	15344	interleukin IL-14	1181-1562
ESh	136052	thrombopoietin (MGDF/Mpl ligand)	230-613
E1:	M10051	insulin receptor	3274-3758
E2;	M17778	uromodulin	1463-1913
F2;	M21121	RANTES pro-inflammatory cytokine	180-545
<u>- 4</u>	M21574	PDGF-alpha receptor	5118-5583
717	M21616	PDGF-beta receptor	842-1133
L 1 A	M22488	bone morphogenetic protein 1	702-1098
1 LN	>>: 13.W		

TABLE 1 (CONT)

			Docition
Array Coordinate		Gene Name	rosmon
F2I	M22489	bone morphogenetic protein 2a	766-796
F2m	M22491	bone morphogenetic protein 3	1458-1731
F2n	M23452	macrophage inflammatory protein GOS19-1	243-704
F3a	M24545	monocyte chemotactic and activating factor MCAF	36-384
F3b	M25667	neuronal growth protein GAP-43	747-1154
F3c	M27288	oncostatin M	833-1113
F3d	M30704	amphiregulin AR	511-837
F3e	M31145	insuline-like growth factor binding protein 1	476-861
E11	M31165	TNF-inducible hyaluronate-binding protein TSG-6	320-584
F3f	M32977	heparin-binding vascular endothelial growth factor VEGF	198-622
A2b	M35410	insuline-like growth factor binding protein 2	680-1071
F7a	M36717	ribonuclease/angiogenun inhibitor RAI	713-1028
F3a	M37722	bFGF receptor	1746-1967
Boh	M57230	glycoprotein gp130	1757-2152
F3h	M57399	nerve growth factor HBNF-1	602-847
F3i	M57502	secreted protein I-309	205-397
F6i	M57765	interleukin IL-11	132-460
E1m	M59818	granulocyte colony-stimulating factor receptor G-CSFR1	1453-1891
F3i	M59964	stem cell factor	898-1283
F3K	M60278	heparin-binding EGF-like growth factor	1905-2146
F3	M60718	HGF (hepatocyte growth factor)	1549-1970
F3m	M60828	keratinocyte growth factor	419-766
F3n	M61176	brain-derived neurotrophic factor BDNF	982-1265
F4a	M62302	growth/differentiation factor GDF-1	615-957
E1n	M62505	C5a anaphylatoxin receptor	725-1098
E5e	M63928	T cell activation antigen CD27	513-977
F4b	M65199	endothelin ET2	338-570
F6i	M65290	interleukin IL-12 (NKSF p40)	622-848
F6k	M65291	interleukin IL-12 (NKSF p35)	066-009
C2b	M67454	Fas antigen	2063-2288
E2a	M68932	Interleukin 8 receptor alpha (IL8RA)	1179-1370
E2b	M73482	NMB-R (neuromedin B receptor)	282-544
F4c	M74178	hepatocyte growth factor-like protein	1643-2015
A5c	M76125	AXL tyrosine kinase receptor	2054-2328
E5f	M83554	lymphocyte activation antigen CD30	3152-3421
F4d	M92381	thymosin beta-10	40-342

TABLE 1 (CONT)

			Docition
Array Coordinate	GeneBank #	Gene Name	1051001
F4e	M92934	connective tissue growth factor	1459-1/48
C2c	M93426	tyrosine phosphatase receptor zeta-polypeptide	5090-1748
ΕΔf	M96956	TDGF3	1294-1712
F2c	S59184	RYK=related to receptor tyrosine kinase isolog	1760-1968
A2c	U01134	VEGF receptor	1288-1604
F2d	U01839	Duffy blood group antigen (Fya-b+)	127-150
A5d	U02687	growth factor receptor tyrosine kinase STK-1	2491-2965
F30	U03187	interleukin 12 receptor component	1053-1381
		monocyte chemoattractant protein 1 receptor (MCP-1RA) alternatively	
F2e	U03882	spliced	1514-1799
		monocyte chemoattractant protein 1 receptor (MCP-1RB) alternatively	
F2f	003905	spliced	1362-1713
C24	U04806	FLT3/FLK2 ligand	29-362
EAn	110117	endothelial-monocyte activating polypeptide II	272-304
F20	U11814	keratinocyte growth factor receptor	753-1189
CSe	U13737	cysteine protease CPP32 isom alpha	2007-2434
SES ERI	1114407	interleukin IL-15	338-695
ESh	1114722	activin type I receptor	333-740
Edh	1143142	VRP (vascular endothelial growth factor related protein)	1165-1559
EVI	X02530	IFN-gamma-inducible chemokine IP-10	280-613
777	X05182	c-kit proto-oncogene	37-430
	X06233	MRP-14 (calcium binding protein in macrophages MIF-related)	16-254
1 - 1 EAk	X06234	MRP-8 (calcium binding protein in macrophages MIF-related)	37-351
FAI	X06374	platelet-derived growth factor A chain PDGF-A	522-955
F4m	X13967	leukemia inhibitory factor LIF	1810-2239
F6m	X17543	interleukin IL-9 (P40)	156-186
F2i	X17648	granulocyte-macrophage colony-stimulating factor receptor GM-CSFRa	868-1173
F4n	X51943	fibroblast growth factor FGF-1	1131-1502
F5a	X53655	nerve growth factor NGF-2 (same as NT-3)	112-416
F5h	X53799	macrophage inflammatory protein-2alpha (MIP2alpha)	157-501
12 L	X54936	PIGF (placenta growth factor)	1098-1371
F4a	X59770	interleukin 1 receptor type II	842-1244
F9i	X60592	Cdw40	198-605
FOK	X72304	beta-thromboglobulin-like protein	230-533
E54	X78686	neutrophil-activating peptide ENA-78	65-329
F5e	X79929	OX40 ligand/gp34	329-657
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TABLE I (CONT)

Array Coordinate G F5f Y F5f Y E2i D D D D D D C5i D E5q D D E5q D D E5q D D D E5q D D D D D D D D D	GeneBank #	Gene Name	LOSINO
		LCICCI	
	Y00787	monocyte-derived neutrophil chemotactic factor MDNCF	787-66
	D10495	protein kinase C delta-type	1467-1817
	D13316	transcription factor E4TF1-47	965-1175
	D13318	transcription factor E4TF1-60	1069-1512
	D13804	recA-like protein HsRad51	867-1159
	D13866	alpha-catenin	2235-2577
	D13889	HI-PI	83-433
	D15050	transcription factor AREB6	2417-2680
	D15057	DAD-1	124-334
	D17517	sky Sky	2132-2597
	D21878	BST-1	706-980
-	D26120	ZFM1 protein	2367-2704
	D26121	ZFM1 protein alternatively spliced product	440-908
	D26155	transcriptional activator hSNF2a	3917-4258
	D26309	LIMK (LIM kinase)	2810-3157
	D28118	DB1	1166-1481
	D28468	DNA-binding protein TAXREB302	386-811
	J03132	intercellular adhesion molecule-1 (ICAM-1)	1220-1599
	J03241	transforming growth factor-beta 3 (TGF-beta3)	1416-1833
	J03634	erythroid differentiation protein (EDF)	983-1372
	J04536	sialophorin (CD43)	178-392
	L04791	excision repair protein ERCC6	1772-2194
	L05624	MAP kinase kinase	842-1217
	L07540	replication factor C 36-kDa subunit	708-1051
	L07541	replication factor C 38-kDa subunit	438-762
-	L08424	achaete scute homologous protein (ASH1)	1113-1455
	L11353	moesin-ezrin-radixin-like protein	355-674
	L11672	Kruppel related zinc finger protein (HTF10)	107-555
	L13616	focal adhesion kinase (FAK)	2179-2631
	L13738	activated p21cdc42Hs kinase (ack)	758-1184
	L13740	TR3 orphan receptor	818-1077
	114611	transcription factor RZR-alpha	620-982
	L14837	tight junction (zonula occludens) protein ZO-1 (tumor suppressor)	6327-6660
	_16785	c-myc transcription factor (puf)	69-351
	L19067	NF-kappa-B transcription factor p65 subunit	1897-2137
B7h	L19185	natural killer cell enhancing factor (NKEFB)	348-736

TABLE 1 (CONT)

			Docition
Array Coordinate	-	Gene ivanie	449 990
D3q	L19606	paired box homeotic protein (PAX8)	113-338
C5m	L20046	ERCC5 excision repair protein	1374-1638
R3h	L20320	protein serine/threonine kinase stk1	89-305
B3c	L20321	protein serine/threonine kinase stk2	2534-2802
B3d	L20422	14-3-3n protein	163-671
D3h	L20433	octamer binding transcription factor 1 (OTF1)	3275-3583
E5!	L20815	S protein	1677-2107
B1a	L20977	plasma membrane calcium ATPase isoform 2 (ATP2B2)	3861-4236
B3e	L22075	guanine nucleotide regulatory protein (G13)	1073-1376
C2h	L22474	Bax beta	227-278
C5n	L24564	Rad	489-780
R3f	L24959	calcium/calmodulin dependent protein kinase	969-1220
B30	L25259	CTLA4 counter-receptor (B7-2)	496-722
	L29511	GRB2 isoform	355-573
D3i	L31881	nuclear factor I-X	415-729
B3h	L32976	protein kinase (MLK-3)	970-1283
A50	L33264	CDC2-related protein kinase (PISSLRE)	454-755
D3i	L34587	RNA polymerase II elongation factor SIII p15 subunit	115-354
B3i	L35233	autocrine motility factor receptor (AMFR)	1221-1514
A2h	M13150	mas proto-oncogene	262-726
D3K	M14631	guanine nucleotide-binding protein G-s alpha subunit partial cds	824-1120
B1b	M15800	MAL protein	461-695
D31	M16937	homeobox c1 protein	367-667
F5k	M21097	differentiation antigen (CD19)	740-1071
B3i	M22199	protein kinase C alpha-polypeptide (PKCA)	767-1106
ESI	M23197	differentiation antigen (CD33)	885-1141
A5h	M26708	prothymosin alpha (ProT-alpha)	538-864
B3k	M28210	GTP-binding protein (RAB3A)	288-591
B3I	M28211	GTP-binding protein (RAB4)	255-495
B3m	M28212	GTP-binding protein (RAB6)	59-310
B3n	M28213	GTP-binding protein (RAB2)	56-269
B4a	M28214	GTP-binding protein (RAB3B)	322-621
B4b	M28215	GTP-binding protein (RAB5)	447-672
A5i	M28882	MUC18 glycoprotein	1756-2180
D3m	M29038	stem cell protein (SCL)	2804-3086
120	M29142	myeloblastin	312-693

TABLE 1 (CONT)

Array Coordinate	_		
State of the state	GeneBank #	Gene Name	Position
E5m	M30257	vascular cell adhesion molecule 1	1056-1450
E5n	M30640	endothelial leucocyte adhesion molecule I (ELAM1)	2098-2549
Cba	M30938	Ku (p70/p80) subunit	2340-2764
A2i	M31213	papillary thyroid carcinoma-encoded protein	2285-2631
D3n	M31523	transcription factor (E2A)	2277-2685
B4c	M31630	cyclic AMP response element-binding protein (HB16) 3' end	316-636
2.5 C6b	M31899	DNA repair helicase (ERCC3)	2109-2466
C6c	M32865	Ku protein subunit	1729-1974
E6a	M33374	cell adhesion protein (SQM1)	53-354
E6b	M34064	N-cadherin	942-1299
B4d	M34356	active transcription factor CREB	433-780
D4a	M34960	transcription factor IID	561-843
Ced	M36089	DNA-repair protein (XRCC1)	1226-1539
B4e	M36429	transducin beta-2 subunit	443-789
B4f	M36430	transducin beta-1 subunit 3' end	58-338
D4b	M36542	lymphoid-specific transcription factor	647-942
D4c	M36711	sequence-specific DNA-binding protein (AP-2)	950-1211
A2i	M54915	h-pim-1 protein (h-pim-1)	893-1187
E6c	M54992	B cell differentiation antigen	963-1224
E6d	M59040	cell adhesion molecule (CD44)	1158-1408
A2k	M60915	neurofibromatosis protein type I (NF1)	740-1027
D4d	M62397	colorectal mutant cancer protein	3626-3902
D4e	M62810	mitochondrial transcription factor 1	640-668
D4f	M62829	transcription factor ETR103	989-1276
D4a	M62831	transcription factor ETR101	1018-1410
Cée	M63488	replication protein A 70kDa subunit	1498-1838
A5k	M63618	bullous pemphigoid antigen	5680-6055
D4h	M63896	transcriptional enhancer factor (TEF1) DNA	2935-3238
E6e	M74387	cell adhesion molecule L1 (L1CAM)	3197-3483
Cef	M74524	HHR6A (yeast RAD 6 homologue)	175-433
E6f	M74777	dipeptidyl peptidase IV (CD26)	1205-1507
C2j	M74816	sulfated glycoprotein-2 3'end	709-990
D4i	M75952	homeobox protein (HOX-11)	1209-1552
D4i	M76541	DNA-binding protein (NF-E1)	706-1053
D4K	M76766	transcription factor (TFIIB)	407-769
D4	M80627	HEB helix-loop-helix protein (HEB)	3676-3984

TABLE 1 (CONT)

			Docition
Array Coordinate	GeneBank #	Gene Name	r Ushinon
D4m	M81601	transcription elongation factor (SII)	CEC-122
A2I	M81750	myeloid cell nuclear differentiation antigen	549-873
A51	M81757	S19 ribosomal protein	113-408
DAn	M81840	NRL gene product	946-1158
0.5a	M83234	nuclease-sensitive element DNA-binding protein	790-1099
Cok	M84820	retinoid X receptor beta (RXR-beta)	643-1135
Cen	M87338	replication factor C 40-kDa subunit (A1)	882-1286
Ceh	M87339	replication factor C 37-kDa subunit	98-355
DSP DSP	M87503	IFN-responsive transcription factor subunit	1057-1520
050	M92299	homeobox 21 protein (HOX2A)	1718-1945
DEG	M92843	zinc finger transcriptional regulator	892-1271
DSG	M93255	FLI-1	728-1118
Doe	MOSARO	follicle stimulating hormone receptor	1507-1752
7.4e	M96824	nucleobindin precursor	701-1068
200	MOGOAA	B-cell specific transcription factor (BSAP)	2446-2771
USB DEb	M97287	MAR/SAR DNA binding protein (SATB1)	1921-2226
USII DEi	M97676	(region 7) homeobox protein (HOX7)	1091-1450
EAb	S64045	5HT1a=5-hydroxytryptamine receptor {transmembrane regions 5 and 6}	128-413
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1101160	transmembrane 4 superfamily protein (SAS)	98-409
240	1102081	quanine nucleotide regulatory protein (NET1)	1079-1323
D4g	1102082	quanine nucleotide regulatory protein (tim1)	1852-2185
D411	1102326	clone ndf43 neu differentiation factor	1430-1701
Del.	1102368	PAX3/forkhead transcription factor fusion	2231-2569
אנים ב	1102619	TFIIIC Box B-binding subunit	5023-5369
DE	1102683	alpha palindromic binding protein	1630-2062
A2m	1103056	tumor suppressor (LUCA-1)	2039-2444
DSn	1103494	transcription factor LSF	1358-1681
B4i	U03688	dioxin-inducible cytochrome P450 (CYP1B1)	1212-1556
Dea	U04847	lini	125-538
Deh	105040	FUSE binding protein	1002-1339
450 450	1105340	p55CDC	1236-1522
BAi	1105875	clone pSK1 interferon gamma receptor accessory factor-1 (AF-1)	1702-2039
7	107139	voltage-gated calcium channel beta subunit	2008-2383
278	1107236	mutant lymphocyte-specific protein tyrosine kinase (LCK)	930-1207
AGa	U07616	amphiphysin	1740-2143
Da la	1107707	epidermal growth factor receptor substrate (eps15)	1828-2140

TABLE 1 (CONT)

		- Indiana and the second and the sec	
Array Coordinate	GeneBank #	Gene Name	Position
E6g	U07819	contactin 1 precursor (CNTN1)	2735-3130
D6c	U08015	NF-ATc	2039-2374
D9Q	U08191	R kappa B	4657-4920
Dée	U08853	transcription factor LCR-F1	1575-1928
B4m	U09564	serine kinase	487-833
Def	U09579	melanoma differentiation associated (mda-6)	1745-2063
B4n	U09607	JAK family protein tyrosine kinase JAK3	3556-3892
Dea	U10323	nuclear factor NF45	967-1380
Deh	U10324	nuclear factor NF90	2901-3146
Dei	U10421	HOX A1 homeodomain protein (HOXA1)	132-492
Dei	U12535	epidermal growth factor receptor kinase substrate (Eps8)	2293-2645
CSI	U13021	positive regulator of programmed cell death ICH-1L (Ich-1)	851-1218
Dek	U13897	homolog of Drosophila discs large protein isoform 1 (hdlg-1)	2248-2624
Del	U14575	(ard-1)	665-942
D6m	U14755	LIM domain transcription factor LIM-1 (hLIM-1)	479-759
Den	U15979	(dlk)	1090-1403
B5a	U16031	transcription factor IL-4 stat	1816-2118
Cei	X06745	DNA polymerase alpha-subunit	3721-4093
A2n	X07024	X chromsome CCG1 protein inv in cell proliferation	4002-4343
A3a	X15218	ski oncogene	2354-2662
A3b	X15219	sno oncogene snoN protein ski-related	2224-2652
E6h	X16841	N-CAM (a nontransmembrane isoform) from skeletal muscle	2338-2646
A3c	X51630	Wilms tumor WT1 zinc finger protein Krueppel-like	1866-2254
D7a	X55122	GATA-3 transcription factor	1097-1383
A6b	X55504	P120 antigen	1970-2245
D7b	X59738	ZFX put transcription activator isoform 1	749-1113
D7c	X67951	proliferation-associated gene (pag)	543-856
B5b	X70326	MacMarcks	638-1008
B5c	X74979	TRKE	2138-2411
E6i	Z26317	desmoglein 2	2819-3135
F7c	A00914	angiotensin-converting enzyme (ACE)	2123-2483
F7d	A06925	relaxin H2	123-427
F7e	D10232	renin-binding protein	289-589
E4i	D28538	glutamate receptor type 1 subtype 5a	3745-4027
F7f	J04040	glucagon	201-540
E4j	L19058	glutamate receptor 5	2514-2779

TABLE 1 (CONT)

	# 21:00	Cone Name	Position
Array Coordinate	Genebank #		828-1183
F7g	M13981	inhibin A-subunit	070-1100
F7h	M14200	diazepam binding inhibitor	6/-25/
F4k	M15169	Beta-2-adrenergic receptor	2412-2783
F41	M29066	dopamine d2 receptor	1226-1521
F7;	M31159	growth hormone-dependent insulin-like growth factor-binding protein	451-744
F7i	M68867	retinoic acid-binding protein II	489-863
F4m	M76446	alpha A1 adrenergic receptor	1599-1942
E4n	M86841	serotonin receptor type 2	938-1239
F7k	U06863	follistatin-related protein precursor	1093-1425
F7I	X58022	corticotropin-releasing factor-binding protein	853-1140
Abc	HT0121	cyclin-dependent kinase 2	1774-2180
A6d	HT0191	cell division cycle protein 25A tyrosine phosphatase	1632-1978
AGe	HT0285	cyclin D3	537-894
Cei	HT330	single-stranded DNA-binding protein pur-alpha	563-855
46	HT0609	cyclin A	876-1218
Zek Zek	HT767	DNA topoisomerase I	2388-2796
) I	HT784	DNA topoisomerase II alpha	2459-2883
Chm	HT1104	6-O-methylguanine-DNA methyltransferase	241-546
260	HT1175	DNA excision repair protein ERCC2 5' end	1520-1821
Δ3η	HT1426	prohibitin	172-455
A30	HT1436	proto-oncogene raf	1704-1989
Com	HT1483	qlutathione reductase	719-1057
02111	HT1489	proto-oncogene c-abl tyrosine protein kinase alt transcript 1	3240-3612
A60	HT1547	cyclin D1	3427-3784
Con	HT1790	qlutathione S-transferase 12	72-420
C7a	HT1848	DNA excision repair protein ERCC1 alt transcript 1	625-938
C3a	HT2041	glutathione S-transferase M1	504-906
C3b	HT2042	glutathione S-transferase pi	203-511
C3c	HT2168	glutathione S-transferase A1	257-583
A6h	HT2181	cyclin D2	3932-4284
A3n	HT2291	proto-oncogene c-src1 tyrosine kinase domain	893-1189
A3h	HT2788	proto-oncogene rel	1357-1605
A3i	HT2856	proto-oncogene rhoA multidrug resistance protein	290-572
C3d	HT2859	glutathione peroxidase	454-745
A3i	HT3039	proto-oncogene shb src-2 homolog	1365-1657
C3e	HT3190	apoptosis regulator bcl-x	412-676

TABLE 1 (CONT)

Array Coordinate GeneBank # C7b HT3218 C7c HT3337 A6i HT3410 A3k HT3563 C3f HT3614 C7d HT4209 C7e HT4247 A6j HT4540 C3g HT4547 C3h HT4547 C3h HT4547 C3h HT4547 C3h HT4547 E6j J02703 E6k J04145 F6i J05633		Gene Name superoxide dismutase 1 cytosolic DNA mismatch repair protein hmlh1	198-486 1765-2020	
		h1	1765-2020	ĺ
			1/65-2020	
		otide exchange factor	3372-3651	
		tumor suppressor DCC colorectal	3749-4042	
		cytochrome P450 reductase	789-1082	
		xeroderma pigmentosum group C repair complementing protein	L	
			282-882	
		na pigmentosum group C repair complementing protein HHR23A	355-632	
		cyclin H	47/1/26	
		glutathione S-transferase T1	617-914	
		ionizing radiation resistance-conferring protein	856-1114	
		endothelial membrane glycoprotein IIIA (GPIIIA)	2038-2373	
		nei trophil adherence receptor alpha-M subunit	2888-3183	
		integrin beta-5 subunit	2279-2528	
		integrin alpha 4 guhlinit	2709-3063	
		Integral alpha + Second (I EA-1/MAC-1/P15095 family) beta subunit	2367-2664	
E6n M15395	9	leukocyte auriesioni protein (Er A. Million III.)	268-639	
E7a M34480	_	plateiet glycoprotein no (or no)	1619-1901	
E7b M35198,	8, J05522	Integrin 6-b	2562-2944	
E7c M59911	_ \	integrin alpha-3 chain	88-271	
E7d M81695,	5, Y00093	leukocyte adhesion glycoprotein P15095	7367	
F7e X06256	3	fibronectin receptor alpha subunit	2094-2367	
	G	fibronectin receptor beta subunit	2116-2482	
		integrin alpha 6	3642-3988	
	7	integrin beta 4	5357-5697	
		integrin alpha subunit	2690-2976	
F71 X74295	ן ע	alpha 7B integrin	255-591	
		leukocyte-associated molecule-1 alpha subunit (LFA-1 alpha subunit)	4526-4856	
	2	Fas ligand	516-840	
		heat-shock protein 40	1400-1782	
		transcription factor SP1 3' end	1876-2272	
		Inrotein kinase C theta (PKC)	2306-2601	
	3 0	protein kinase (JNK1)	952-1263	
		CDK4.inhihitor (n16-INK4)	482-836	
		CDIVE-Illinois (P10 inv.)	925-1204	
	3	D30 IIIIUgeli activated protein (mor) / minasc	790-1169	
B5g L36719	6	MAP Kinase Kinase 3 (MKN3)	2788-3103	
B5h L36870	0	MAP kinase kinase 4 (MKK4)	2010-0013	

TABLE 1 (CONT)

			Docition
Array Coordinate	GeneBank #	Gene name	TOSHIOII
Sj.	M13228	N-myc oncogene protein	/61-1188
A3	M15400	retinoblastoma susceptibility	2839-3101
A3m		c-yes-1	1325-1676
BSi		"lyn, tyrosine kinase"	1393-1666
A3n	M19720	L-myc protein	5847-6118
A4a	M19722	far proto-oncogene encoded p55-c-fgr protein	521-856
A6I		cyclin B	979-1311
BSi		protein kinase C (PKC) type beta I	1561-1821
BSK	M31158	cAMP-dependent protein kinase subunit RII-beta	1305-1506
B7;	M34664	chaperonin (HSP60)	533-839
B5	M35203	protein-tyrosine kinase (JAK1)	2768-3054
C7f	M60974	growth arrest and DNA-damage-inducible protein (gadd45)	526-886
RSm	M65066	cAMP-dependent protein kinase regulatory subunit RI-beta 3' end	444-662
A6m	M73812	cyclin E	1295-1658
A4h	M74088	ÁPC	7992-8326
D7e	M83221	I-Rel	853-1129
RSn	M84489	extracellular signal-regulated kinase 2	1241-1522
DZf	M97190	Sp2 protein	396-682
D70	M97191	Sp3 protein	1588-1987
CZo	S40706	GADD153=growth arrest and DNA-damage-inducible	480-789
Cak	U25994	cell death protein (RIP)	848-1123
BGa	U30473	putative src-like adapter protein (SLAP)	524-901
17.7h	U35835	DNA-PK	2250-2680
A6n	U40343	CDK inhibitor p19INK4d	750-952
F71	U43522	cell adhesion kinase beta (CAKbeta)	3658-3952
A4c	U43746	breast cancer susceptibility (BRCA2)	10056-10346
A7a	U47413	cyclin G1	755-1035
A7b	U47414	cyclin G2	989-1254
A7c	U66838	cyclin A1	1205-1456
A4d	X02751	N-ras	708-1064
B7k	X07270	heat shock protein hsp86	380-577
B6b	X07767	cAMP-dependent protein kinase catalytic subunit type alpha (EC 27137)	460-740
A4e	X16706	fra-2	376-663
A4f	X16707	fra-1	617-897
A40	X51521	ezrin	1611-1883
B71	X54079	heat shock protein HSP27	423-683

TABLE 1 (CONT)

			Docition
Array Coordinate	GeneBank #	Gene Name	Position
Ber	X54637	tyk2 non-receptor protein tyrosine kinase	3/8/-4110
2000	X5 1551	Quili	508-780
A4n	ASSOCIA	Series Se	488-876
A4i	X55456	EBK1 protein serine/threonine kinase	754-1094
Bed	X60188		806-1267
B6e	X80692	THAS TITLES TO THE STATE OF THE	865-1239
C3I	X86779	FAST Kinase	2061-2463
E7m	X87838	Deta-catenin	935-1200
C3m	X89986	NBK apoptotic inducer protein	30-937
A7d	X92669	p35 cyclin-like CAK1-associated protein	3001-3083
B6f	Z29090	phosphatidylinositol 3-kinase	5021-3203
C3	L11015	lymphotoxin-beta	638 1000
Bhn	L31951	protein kinase (JNK2)	1020-1000
Beh Beh	L34583	tyrosine phosphatase (clone HFAP10)	13/2-1/01
CAa	L41690	TNF receptor-1 associated protein (TRADD)	1009-1313
CAP.	M14745	bcl-2	5087-5362
040	1115172	NIP1 (NIP1)	412-/19
245	1145174	NIP3 (NIP3)	272-63/
C40	1120637	cysteine protease MCH2 isom beta (MCH2)	387-697
C4e	02033/	BAK protein	1371-1661
C4f	U23/65	DAN proteins	763-1107
C4g	U28014	cysleme protease (10th 1tt m)	64-293
C4h	U29680	A1 protein	1018-1413
B6i	U34819	JNK3 alphaz protein kiliase (olynorz)	1444-1848
C4i	U45878	Inhibitor of apoptosis protein 1	2000-2363
C4j	U45879	inhibitor of apoptosis protein 2	266-621
C4K	U45880	X-linked inhibitor of apolosis protein Aixi	986-1289
C41	U56390	cysteine protease ICE-LAPO	211-616
C4m	U57059	Apo-2 ligand	2276-2690
C4n	U60519	apoptotic cysteine protease incit (incit)	1327-1607
C5a	U60520	apoptotic cysteine protease inclib isoni alpiia (mons)	478-695
B6i	X14454	interferon regulatory factor 1	2770
CSb	X96586	FAN protein	4407 4674
C5c	Y09392	WSL-LR WSL-S1 and WSL-S2 proteins	1407-1071
D7h	D11117	homeobox HOX 4A homeodomain protein	4200-4447
A70	D38305	Tob	926-929
150	D42108	phospholipase C	1635-2003
DOK	D45130	zinc-finger DNA-binding protein	5113-5551
1/0	101010		

TABLE 1 (CONT)

			Docition
Array Coordinate	GeneBank #	Gene Name	4702 2000
ESa	D49394	serotonin 5-HT3 receptor	1/03-2000
L.3a	1 16/6/	ETS oncodene (PEP1)	418-711
A4J	1.00046	CI K2	1106-1356
A/1	128210	CLK3	551-1002
A7g	1,5550	OEK3	144-459
A7h	L29222	NIMPA sociator	2097-2395
E5b	L76224	INMIDA Feception	1962-2225
B7m	M11717	near snock protein (v)	652-919
F5g	M27544	insulin-like growth factor	8035-8423
Bel	M68516	protein C inhibitor	701-1070
F5h	M86528	neurotrophin-4 (NT-4)	486-837
B6m	U09578	MAPKAP kinase (3pK)	1259-1502
A7i	U10564	CDK tyrosine 15-kinase WEETHU (WEETHU)	1528-1733
C7i	U12134	UNA damage repair and recombination protein traduct	175-566
B6n	U14187	receptor tyrosine kirjase ligariu LETIN-9 (E. EGG)	169-436
B7a	U14188	receptor tyrosine kinase LEDN-4 (ET LC4)	1119-1453
B7b	U18087	335-CAMP phosphodiesierase nr DE-4A0	980-1322
C5d	U21092	CD40 receptor associated racior 1 (Charlet)	1048-1316
A7i	U22398	CDK-inhibitor P3/KIP2 (KIP2)	488-796
A4k	U24166	EB1	3054-3444
A4I	U26710	CBL-B	2226 2606
D7i	U28838	transcription factor TFIIIB 90 kDa subunit (HTFIIIB90)	230-2002
D7k	M30504	transcription initiation factor LFIID subunit LAFII31	200-000
EBn	U32659	IL-17	0/0-/07
5 2	1132944	cytoplasmic dynein light chain 1 (hdlc1)	48-265
0.00	1133635	colon carcinoma kinase-4 (CCK4)	3507-3784
D/C	1133841	ataxia telangiectasia (ATM)	8938-9135
() () () () () () () () () ()	1135735	RACH1 (RACH1)	1072-1391
7/7	1139613	cysteine protease ICE-LAP3	541-844
C21	1139657	MAP kinase kinase 6 (MKK6)	1060-1389
B/0	1140000	integrin-linked kinase (ILK)	1245-1530
B7e	040202	7.7	143-356
A7I	041816	Etc transcription factor (NFRF-2)	1967-2400
D7I	043188	Les italiscription racio (1967)	1455-1849
B7f	U43408	typositie Mitase (Tint)	1417-1679
A4m	U57456	Italisionimig growni ractor beta signaming process.	121-403
C5g	U59747	BCI-W (DCI-W)	674-887
l)7m	U59863	HAF-Interacting protein 1-1 hAr	

TABLE 1 (CONT)

Array Coordinate GeneBank #	GeneBank #	Gene Name	Position
E7n	U60800	semaphorin (CD100)	2517-2921
A4n	U61262	neogenin	3144-3573
C7k	U63139	Rad50 (Rad50)	5117-5435
A5a	U68162	thrombopoietin receptor (MPL)	2184-2448
CSh	U71364	serine proteinase inhibitor (P19)	618-986
C7I	X83441	DNA ligase IV	2787-3074
C7m	X84740	DNA ligase III	2460-2780
C7n	X90392	DNase X	2038-2427
B7n	HT4197	glutaredoxin	43-325
F7m	U08098	estrogen sulfotransferase (STE)	533-852
F7n	X54469, M28019	beta-preprotachykinin	321-7888
B7g	L25876	protein tyrosine phosphatase (CIP2)	110-499
A7m	M81934	CDC25B	2286-2602
A7n	U17075	P14-CDK inhibitor	116-462
G12	X01677	LIVER GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE	663-932
G13	K00558	TUBULIN ALPHA	
		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN	
G14	M11886	[MHC]	
G19	X00351	BETA-ACTIN	692-1077
G20	X56932	23 kDa HIGHLY BASIC PROTEIN	
G21	U14971	RIBOSOMAL PROTEIN S9	
G5	M26880	UBIQUITIN	1922-2181
95	M86400	PHOSPHOLIPASE A2	
G7	V00530	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE	

Mouse Array

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In the mouse array according to the subject invention, all of the unique polynucleotide probe compositions will correspond to a mouse gene of interest. Mouse genes that are represented on the array are key genes, by which is meant that they have been reported to play primary roles in a variety of different biological processes. Typically the mouse genes represented on the array are genes that are under tight transcriptional control. Genes of interest that may be represented on the array include: oncogenes, cell cycle genes, apoptosis genes, growth factor genes, cytokine genes, interleukin genes, receptor genes, and genes associated with different stages of embryonic development.

In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: oncogenes & tumor suppressors; cell cycle regulators; stress response proteins; ion channel & transport proteins; intracellular signal transduction modulators & effectors; apoptosis-related proteins; DNA synthesis, repair & recombination proteins; transcription factors & general DNA binding proteins; growth factor & chemokine receptors; interleukin & interferon receptors, hormone receptors; neurotransmitter receptors; cell-surface antigens & cell adhesion proteins; interleukins & interferons; cytoskeleton & motility proteins; and protein turnover. In a specific mouse array of interest, the spots are as

listed in Table 2.

The mouse array of the subject invention finds use in a variety of different applications, where such applications include: profiling differential gene expression in transgenic knockout mice or other experimental mouse models; investigating processes such as embryo genesis and tumorigenesis; discovering potential therapeutic and diagnostic drug targets; and the like.

TABLE 2

GenBank # Gene Name	Gene Name	Array Coordinate	Position
040470	Man Dudet . want DNIA ramair protein Dadet and E anii Dana Apamalama	# G	055 1100
D134/3	IMILINAUDI, yeast DIVA lepail proteili naubi allu E coll neca nomogue.	COIII	6511-000
D17630	Interleukin-8 receptor	E3h	664-1022
D25281	Catenin alpha	E5m	1276-1594
D31788	BST-1; lymphocyte differentiation antigen CD38	B2h	674-1014
D31942	Oncostatin M	F3n	1017-1360
L05630	C5A receptor	E1g	841-1165
L07264	Heparin-binding EGF-like growth factor (Diphtheria toxin receptor)	F2d	258-673
U04807	Fms-related tyrosine kinase 3 Flt3/Flk2 ligand	C3i	46-418
L24495	CD27; lymphocyte-specific NGF receptor family member	C2I	596-846
M28998	Fibroblast growth factor receptor Basic (b FGF-R)	E2c	200-583
M58288	Granulocyte colony - stimulatings factor receptor	E1j	251-529
M62301	Growth/ diffferentiation factor 1 (GDF-1) (TGF- beta family)	F2b	2267-2566
M69042	PKC-delta; protein kinase C delta type	B6g	1740-2011
M74517	GA binding protein beta-2 chain	D3d	613-931
M83312	CD 40L receptor (TNF receptor family)	E1f	417-754
M83649	Fasl receptor (Fas antigen, Apo-1 antigen)	C3f	416-736
M86671	Interleukin 12 (p40) beta chain	F4n	652-963
M95200	Vascular endothelial growth factor (VEGF)	F4j	688-955
U03421	Interleukin 11 (adipogenesis inhibitory factor)	F4m	196-475
U14332	Interleukin 15	F5a	605-1057
U15159	LIMK; LIM serine/threonine kinase	B5I	1376-1699
U83628	DAD-1; defender against cell death 1	C3d	221-509
1125416	CD 301 receptor (1 ymphocyte activation antigene CD 30, Ki-1 antigene)	C2m	135-435
U44725	Mast cell factor	F3i	79-417
	C-C chemokine receptor (Monocyte chemoattractant protein 1 receptor		
U56819	(MCP-1RA)	E1d	965-1262
X06381	Leukemia inhibitory factor (LIF) (cholinergic differentiation factor)	F3d	63-366
X52264	Intercellular adhesion molecule-1	E7i	1053-1385
X59769	Interleukin-1 receptor type II	E2n	883-1134
X72305	Corticotropin releasing factor receptor	Eth	1411-1748
X72307	Hepatocyte growth factor (hepapoitein)	F2e	641-965
Z22703	Keratinocyte growth factor FGF-7	F3b	63-325
Z31663	Activin type I receptor	E1a	847-1130
1			

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
D01034	Transcription factor TF II D	B4j	291-556
	ZO-1; Tight junction protein; discs-large family member, partially		
D14340	homologous to a dlg-A tumor suppressor in Drosophila/	A2d	3714-4001
	ERCC5 excision repair protein; DNA-repair protein complementing XP-G		
D16306	cells (XPG)	Cef	1336-1639
L22472	Bax; Bcl-2 heterodimerization partner and homologue	C1g	172-534
	B7-2; T lymphocyte activation antigen CD86; CD28 antigen ligand 2, B7-2		
L25606	antigen; alternative CTLA4 counter-receptor	B2g	570-967
	NF2; Merlin (moesin-ezrin-radixin-like protein); shwannomin, murine		
L27105	neurofibromatosis type 2 susceptibility protein	A1i	2175-2400
M13945	Pim-1 proto-oncogene	A4a	2713-2930
M20157	Egr-1 Zn-finger regulatory protein	D2i	399-753
M25811	PKC-alpha; protein kinase C alpha type	B6e	1566-1924
M27129	CD44 antigen	E6e	789-1141
M31042	T-lymphocyte activated protein	D6h	285-606
M31131	Neuronal-cadherin (N-cadherin)	E7k	1212-1409
	ATP-dependent DNA helicase II 70 kDa subunit; thyroid Ku (p70/p80)		
M38700	autoantigen p70 subunit; p70 Ku)	C5h	274-632
M63660	G13; G-alpha-13 guanine nucleotide regulatory protein	B6n	2057-2377
M83380	Transcription factor RelB	D7c	1456-1728
M84487	Vascular cell adhesion protein 1	E7m	984-1304
	ERCC3 DNA repair helicase; DNA-repair protein complementing XP-B cells		
S71186	(XPBC)	C6e	1147-1444
S76657	CRE-BP1; cAMP response element binding protein 1	B3l	412-748
U02887	XRCC1 DNA-repair protein, affecting ligation	C7n	900-1183
U53228	Nuclear hormone receptor ROR-ALPHA-1	D5i	368-675
U57311	14-3-3 protein eta	B7g	374-640
X56135	Prothymosin alpha	A7m	186-455
X57487	PAX-8 (paired box protein PAX 8)	DSI	680-1011
X58995	CamK IV; Ca2/calmodulin-dependent protein kinase IV (catalytic chain)	BSf	1269-1608
	ATP-dependent DNA helicase II 80 kDa subunit; thyroid Ku (p70/p80)		
X66323	autoantigen p80 subunit; p80 Ku)	C5i	565-875
X67812	Ret proto-oncogene (Papillary thyroid carcinoma-encoded protein)	A4f	2359-2680
	Nm23-M2; nucleoside diphosphate kinase B; metastasis-reducing protein;		
X68193	c-myc-related transcription factor	C4c	80-454
		1	

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
X97052	MAPKK6; MAP kinase kinase 6(dual specificity) (MKK6)	B6d	375-711
D17384	DNA polymerase alpha catalytic subunit (p180)	CSI	563-908
	Caspase-3; Nedd2 cysteine protease (positive regulator of programmed		
D28492	cell death ICH-1 homologue)	C1b	398-694
D50621	PSD-95/SAP90A	Ded	1512-1889
J04946	Angiotensin-converting enzyme (ACE) (clone ACE.5.)	F6f	850-1113
	Clusterin; complement lysis inhibitor; testosterone-repressed prostate		
L08235	message 2; apolipoprotein J; sulfated glycoprotein-2	C3b	515-744
L12721	Adipocyte differentiation-associated protein	D1c	404-709
121671	Epidermal growth factor receptor kinase substrate EPS8	D2k	1592-1873
L33768	Jak3 tyrosine-protein kinase; Janus kinase 3	B5j	3123-3426
L33779	Desmocollin 2	E6I	1317-1691
L47650	Stat6; signal transducer and activator of transcription 6; IL-4 Stat; STA6	B4g	2057-2411
M12056	Lymphocyte-specific tyrosine-protein kinase LCK	A5a	1205-1488
M22115	ERA-1 Protein (ERA-1-993)	D2I	723-1062
M26283	Homeo Box protein 2.1 (Hox-2.1)	D4a	647-884
M32309	Zinc finger X-chromosomal protein (ZFX)	D7n	2153-2554
M55512	WT1; Wilms tumor protein; tumor suppressor	A2c	1262-1563
M57422	Tristetraproline	B4k	262-504
M96823	Nucleobindin	D5j	80-357
M97013	PAX-5 (B cell specific transcription factor)	D6a	286-629
	IFNgR2; interferon-gamma receptor second (beta) chain; interferon gamma		
Se9336	receptor accessory factor-1 (AF-1)	B3b	832-1089
S74227	Transcriptional enhancer factor 1 (TEF-1)	D7i	934-1233
U02079	Transcription factor NFAT 1, isoform alpha	D7a	1601-1910
U05252	DNA-binding protein SATB1	D2e	1101-1380
	CCHB3; calcium channel (voltage-gated; dihydropyridine-sensitive; L-type)		
U20372	beta-3 subunit)	B2c	351-639
	n57kin9: cdk-inhihitor kin9 (cvclin-dependent kinase inhibitor 1B) member		
U20553	of the p21CIP1 Cdk inhibitor family; candidate tumor suppressor gene	A7g	989-1272
U36203	snoN; ski-related oncogene	E2j	671-1006
X14759	Homeo Box protein 7.1 (Hox-7.1)	D4f	740-992
X14943	Neuronal cell surface protein F3	E7I	1033-1311
X55123	GATA-3 transcription factor	D3f	858-1125

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
X57621	YB1 DNA binding protein	D7j	550-873
X58384	Dipeptidyl peptidase iv	E7f	61-294
X59421	Fli-1 ets-related proto-oncogene	A3b	267-623
X66224	RXR-beta cis-11-retinoic acid receptor	B4c	1225-1477
X78445	C3H cytochrome P450; Cyp1b1	B1j	295-593
X96859	Ubiquitin-conjugating enzyme, yeast Rad6 homologue; murine HR6B	C7k	51-392
227088	Relaxin	C4i	51-365
227410	Transcription factor LIM-1	D6m	1673-1934
D10061	DNA topoisomerase I (Top I)	C5m	1051-1357
D12513	DNA topoisomerase II (Top II)	C5n	520-870
D30687	GST Pi 1; glutathione S-transferase Pi 1; preadipocyte growth factor	C2d	62-369
J03958	Glutathione S-transferase A	C1n	54-311
J04696	Glutathione S-transferase Mu 1	C2b	13-263
L10656	c-Abl proto-oncogene	A4k	878-1145
M13071	A-Raf proto-oncogene	A3k	1042-1320
M17031	c-Src proto-oncogene	A4n	452-758
M35523	Retinoic acid binding protein II cellular (CRABP-II)	D6e	276-571
M83749	Cyclin D2 (G1/S-specific)	A6g	781-1074
U43844	Cyclin D3 (G1/S-specific)	A6h	484-790
S49542	5-Hydroxytryptamine receptor [Serotonin receptor type 2 (5HT2)]	E4e	400-707
S78355	Cyclin D1 (G1/S-specific)	A6f	1858-2205
	Pur-alpha transcriptional activator; sequence-specific ssDNA-binding		
U02098	protein	C7e	1082-1309
U27323	Cdc25a; cdc25M1; MPI1 (M-phase inducer phosphatase 1)	A7j	986-909
X07414	ERCC-1; DNA excision repair protein	Ced	189-484
X15842	c-rel proto-oncogene	A2m	1729-2064
X69618	Inhibin alpha subunit	F2g	810-1117
X76341	Glutathione reductase	C1m	115-377
X81581	Insulin-like growth factor binding protein-3 (IGFBP-3)	F2k	474-719
Z26580	Cyclin A (G2/M-specific)	A6a	701-1009
Z46845	Preproglucagon	A5i	172-531
	NF-kB p65; NF-kappa-B transcription factor p65 subunit; rel-related		
M61909	polypeptide	B4a	101-363
D11091	PKC-theta; protein kinase C theta type	B6h	658-957
D13867	VLA-3 alpha subunit	E7n	288-589

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
D17571	NADPH-cytochrome P450 reductase	C4a	326-605
D17584	Beta-protachykinin a	A5j	273-523
D30743	Wee1/p87; cdc2 tyrosine 15-kinase	A7h	1816-2159
D83966	Protein tyrosine phosphatase	C4g	1060-1429
J05205	Jun-D; c-jun-related transcription factor	A3g	737-964
L23423	Integrin alpha 7	E7e	2399-2713
L28177	Gadd45; growth arrest and DNA-damage-inducible protein	C3j	144-434
L35049	Bcl-xL apoptosis regulator (bcl-x long); Bcl-2 family member	C1j	641-906
X03919	N-myc proto-oncogene protein	A3j	3262-3450
M20473	cAMP-dependent protein kinase type I-beta regulatory chain	B5g	538-750
M21065	IRF1; interferon regulatory factor 1	B7k	1-233
M36830	HSP86; heat shock 86kD protein	B1d	255-551
	LFA1-alpha; integrin alpha L; leukocyte adhesion glycoprotein LFA-1 alpha		
M60778	chain; antigen CD11A (p180)	B3e	1838-2050
M88127	APC; Adenomatous Polyposis Coli protein	A1a	4127-4476
S93521	Cdc25b; cdc25M2; MPI2 (M-phase inducer phosphatase 2)	A7k	1893-2200
U03279	PI3-K p110; phosphatidylinositol 3-kinase catalytic subunit	B6j	1437-1723
003560	HSP27; heat shock 27kD protein 1	Bla	245-500
U05247	Csk; c-Src-kinase and negative regulator	B4n	645-984
	Fast; Fas antigen ligand; generalized lymphoproliferation disease gene		
U06948	(gld) in mice	C3g	168-488
U10871	MAPK; MAP kinase; p38	B5m	465-780
U19597	p19ink4; cdk4 and cdk6 inhibitor	A7d	228-516
U19617	Elf-1 Ets family transcription factor	D2j	1585-1902
U21050	CRAF1; TNF receptor (CD40 receptor) associated factor; TRAF-related	C3c	1225-1466
	SPI3; serpin; similar to human proteinase inhibitor 6 (placental thrombin		
U25844	inhibitor) serine proteinase inhibitor	C4	915-1230
	RIP cell death protein; Fas/APO-1 (CD95) interactor, contains death		
U25995	domain	C4j	1945-2223
U29056	SLAP; src-like adapter protein; Eck receptor tyrosine kinase-associated	B5c	109-427
U43678	Atm; ataxia telangiectasia murine homologue	C5g	8989-9170
U51196	EB1 APC-binding protein	A1e	607-834
U51907	TANK; I-TRAF; TRAF family member associated NF-kB activator	B4h	135-437

TABLE 2 (CONT)

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GenBank #	Gene Name	Array Coordinate	Position
U59463	Caspase-11; ICH-3 cysteine protease; upstream regulator of ICE	C1a	352-686
U59883	MLH1 DNA mismatch repair protein; Mutt. homologue	C6k	1037-1278
X04480	Insulin-like growth factor-IA	F3a	183-406
X07640	Cell surface glycoprotein MAC-1 alpha subunit	Eej	1892-2179
X13664	N-ras proto-oncogene; transforming G-protein	A5e	548-857
X13945	L-myc proto-oncogene protein	A3h	5287-5590
X14951	CD18 antigen beta subunit (leukocyte adhesion LFA-1) (CD3, P150, 95)	E5n	1366-1706
X52191	c-Far proto-oncogene	A4m	1305-1538
X53176	Integrin alpha 4	E7b	2176-2449
X53532	PKC-beta; protein kinase C beta-II type	B6f	1712-2089
	HSP60; heat shock 60 kDa protein 1 (chaperonin, GroEL homologue);		
X53584	mitochondrial matrix protein P1	B1b	1432-1459
X57111	c-Cbl proto-oncogene (Adaptor protein)	A5b	858-1151
X59868	Cdc25 phosphatase; guanine nucleotide releasing protein	A7i	942-1276
	Ezrin; Villin 2; NF-2 (merlin) related filament/plasma membrane associated		
X60671	protein	A1f	1571-1812
X64713	Cyclin B1 (G2/M-specific)	A6c	1184-1447
X69902	Integrin alpha 6	E7d	261-611
X72395	5-Hydroxytryptamine (serotonin) receptor 3	E4j	1422-1711
X73573	Homeobox protein HOXD-3	D4h	141-362
X75888	Cyclin E (G1/S-specific)	A6i	799-1140
X76850	MAPKAPK-2: MAP kinase-activated protein kinase; MAPKAP kinase 2	B5n	719-987
X83971	Fra-2 (fos-related antigen 2)	A3d	617-844
X84311	Cyclin A1 (G2/M-specific)	A6b	656-916
	DCC; netrin receptor; immunoglobulin gene superfamily member; former		
X85788	tumor suppressor protein candidate	A1d	4193-4508
	MHR23A; Rad23 UV excision repair protein homologue; xeroderma		
X92410	pigmentosum group C (XPC) repair complementing protein	Cei	613-955
	MHR23B; Rad23 UV excision repair protein homologue; xeroderma		
X92411	pigmentosum group C (XPC) repair complementing protein	C6j	542-807
Y00769	Integrin beta	E7g	1990-2320
Z32767	MmRad52; yeast DNA repair protein Rad52 homologue	Cen	159-417
Z37110	Cyclin G (G2/M-specific)	A6k	300-619
D13458	Prostaglandin E2 receptor EP4 subtype	B3f	1146-1442
D90205	Interleukin-5 receptor	E3f	1389-1739

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
J00380	Epidermal growth factor (EGF)	F1j	180-505
J04843	Erythropoietin receptor	E2a	1193-1377
J05149	Insulin receptor	E4a	653-1011
K01700	p53; tumor suppressor; DNA-binding protein	A1I	1125-1517
L03529	Cf2r; coagulation factor II (thrombin) receptor	B2j	762-1154
L09562	PTPRG; protein-tyrosine phosphatase gamma	B71	1248-1504
L10075	DNA-binding protein SMBP2	D2f	4790-5088
L12120	Interleukin-10 receptor	E3a	1762-2110
L20048	Interleukin-2 receptor gamma chain	E3c	1073-1313
L24755	Bone morphogenetic protein 1	F1b	2402-2676
L33406	Uromodulin	F4i	1809-2136
L34169	Thrombopoietin	F4e	652-954
M13177	Transforming growth factor beta	F4f	772-1075
M13926	Granulocyte colony- stimulating factor (G-CSF)	F2a	86-377
M14220	Neuroleukin	F3m	1110-1490
M14951	Insulin-like growth factor-2 (somatomedin A)	F2n	46-328
M15131	Interleukin 1 beta	F4k	827-1225
M16449	c-myb proto-oncogene protein	A2k	1212-1513
M16819	Tumor necrosis factor beta TNF-beta (Lymphotoxin-alpha)	F4h	461-805
M20658	Interleukin-1 receptor	C3n	2050-2410
X05010	CSF-1; M-CSF; colony stimulating factor-1	A5g	1268-1657
M27959	Interleukin-4 receptor (membrane-bound form)	E3e	2469-2705
M28233	Interferon-gamma receptor	E2m	1262-1550
M29697	Interleukin-7 receptor	E3g	701-1104
M34815	Gamma interferon induced monokine (MIG)	F1m	42-323
M37897	Interleukin 10	F4I	175-456
M57999	NF-kappa B binding subunit (nuclear factor) (TFDB5)	D5g	3122-3417
M59378	Tumor necrosis factor receptor 1; TNFR-1	CSd	1961-2376
M84607	PDGFRa; platelet-derived growth factor alpha-receptor	A4e	474-803
M84746	Interleukin-9 receptor	E3i	795-1086
M87039	iNOSI; nitric oxide synthase (inducible)	C3m	3178-3455
M89641	Interferon alpha-beta receptor	E2I	808-1120
M94087	Activating transcription factor 4 (mATF4)	D1b	416-769
S56660	Beta2-RAR; retinoic acid receptor beta-2	B3k	589-896
S67051	Tie-2 proto-oncogene	A4i	1843-2179

TABLE 2 (CONT)

# 75000	Cone Name	Array Coordinate	Position
Genbain #	IGEL Rainhar insulin-like growth factor I receptor alpha subunit	C3I	489-885
2000	IGER II: insulin-like growth factor receptor II, cation-independent mannose-		
1104710	6-P receptor; elevated in Wilms's tumor cells	C3k	707-1060
U06922	Stat3; APRF; acute phase response factor	B4e	1575-1910
U18542	Calcitonin receptor 1b	E3k	1375-1630
1132329	Endothelin b receptor [Ednrb]	E1i	279-695
U32330		F4c	703-1008
X04367	Pre-platelet-derived growth factor receptor	E2i	2336-2677
X04836	CD 4 receptor (T cell activation antigene)	E1e	1652-1877
X07962	Interleukin 7	F5d	241-496
X12531	Macrophage inflamatory protein	F3e	25-359
X14432	Thrombomodulin	F4d	1082-1365
X51975	Interleukin 6 (B cell differentiation factor)	F5c	1638-1898
X53779	Androgen receptor	E3j	2189-2491
X56848	Bone morphogenetic protein 4 (BMP-4) (TGF-beta family)	F1d	1275-1513
X57349	Transferrin receptor protein (p90, CD71)	B3h	654-1023
X57413	Transforming growth factor beta 2	F4g	2227-2541
X57497	Glutamate receptor, ionotropic AMPA 1	E5h	1290-1657
X57796	TNF 55: tumor necrosis factor 1 (55kd)	C5b	656-1022
X58876	Mdm2: p53-regulating protein	A1h	1364-1646
X61753	Transcription factor 1 for heat shock gene	D6i	203-570
X65453	CD40L; CD40 ligand	C2n	545-809
	c-Fms proto-oncogene (macrophage colony stimulating factor 1 (CSF-1)		
X68932	receptor)	A4b	2399-2686
X70472	B-myb proto-oncogene; myb-related protein B	A2f	2109-2456
X76654	Ear-2; v-erbA related proto-oncogene	A2n	1065-1376
X80764	Tie-1 tyrosine-protein kinase receptor	B3g	1425-1844
D10651	Glutamate receptor, ionotropic NMDA2B (epsilon 2)	E5j	506-786
D10217	Glutamate receptor, ionotropic NMDA2A (epsilon 1)	E5i	3966-4209
D10329	CD7 antigen	E6g	28-421
D00926	Transcription factor S -II (transcription elongation factor)	DZd	518-767
D12482	Basic Fibroblast growth factor (b- FGF)	F1a	290-620
D16250	Bone morphogenetic protein receptor	E1c	1454-1837
D17292	G-protein-coupled receptor	E2d	833-1115
D17407	Transcription factor SP2	D7g	734-1079

TABLE 2 (CONT)

GonBank #	Gene Name	Array Coordinate	Position
D29678	Cdk5: cvclin-dependent kinase 5	A6n	552-882
D25540	TGF-beta receptor type 1	E2k	1407-1629
D26077	Kinesin like protein KIF 3B	F6a	3519-3722
D29951	Kinesin family protein KIF1A	F5m	2553-2830
D38258	Fibroblast growth factor 9	F1k	91-379
D83698	Neuronal death protein	C4b	627-805
D84372	Svp. SH-PTP2; adaptor protein tyrosine phosphatase	B5e	1229-1543
J03168	Interferon regulatory factor 2 (IRF 2)	D4I	718-976
J02870	Lamimin receptor 1	E7j	368-675
D90176	NF-1B protein (transcription factor)	DSf	452-791
J03236	Jun-B; c-jun-related transcription factor	A3f	514-740
.103520	Tissue plasminogen activator	F7e	622-1020
103770	Homeo Box protein 4.2 (Hox-4.2)	D4e	565-945
104113	Nur77 early response protein; thyroid hormone (TR3) receptor	C4d	825-1059
.104103	Ets-2 transcription factor	D3b	917-1281
J04115	c-Jun proto-oncogene (transcription factor AP-1 component)	A2i	951-1238
.105609	Serine protease inhibitor homolog J6	F71	581-855
K01759	Nerve growth factor beta (beta-NGF)	F3I	642-901
101640	Cdk4; cyclin-dependent kinase 4	A6m	230-616
K02582	Acetylcholine receptor delta submit	E4I	1400-1655
1 02526	MAPKK1; MAP kinase kinase 3 (dual specificity) (MKK1)	B6a	1284-1583
L04662	GABA-A transporter 4	E5g	960-1341
104663	GABA-A transporter 3	ESf	1010-1320
	Vegfr1; Vascular endothelial growth factor receptor 1 / Fms-related tyrosine		
L07297	kinase 1 (Flt1)	A4j	1144-1541
L10084	Adrenergic receptor, beta 1	E4m	404-772
L25890	Eph3 (Nuk) tyrosine-protein kinase receptor	B2k	2255-2491
L16953	MTJ1; DnaJ-like heat-shock protein from mouse tumor	B1e	1059-1384
L19622	TIMP-3 tissue inhibitor of metalloproteinases-3	F7n	274-592
124563	Insulin receptor substrate-1 (IRS-1)	E4b	1027-1304
L13968	YY1 (UCRBP) transcriptional factor	D7k	1052-1292
L28095	Interleukin-converting enzyme (ICE)	F7a	30-269
L38847	Hepatoma transmembrane kinase ligand	F2f	927-1219
L36179	Voltage-gated sodium channel	B2f	4179-4505
L37296	Bad; heterodimeric partner for Bcl-XL and Bcl-2; promotes cell death	C1d	1079-1375

TABLE 2 (CONT)

GenRank #	Gene Name	Array Coordinate	Position
1 35236	Juk stress-activated protein kinase (SAPK)	B5k	795-1032
M11686	Cytoskeletal epidermal keratin (18 human)	F5i	473-773
M11434	Nerve growth factor alpha (alpha-NGF)	F3k	294-494
M10937	Epidermal keratin (1 human)	F5k	326-683
M14537	Nicotinic acetylcholine receptor	E5k	1226-1568
M14757	MDR1; P-qlycoprotein; multidrug resistance protein; efflux pump	B1g	1500-1886
M18934	CD2 antigen	E6a	354-602
M17192	Homeo Box protein 1.1 (Hox-1.1)	D3n	466-723
M19436	Fetal myosin alkali light chain	F5I	205-504
M25892	Interleukin 4	F5b	77-310
	Rb; pp105; Retinoblastoma susceptibility-associated protein (tumor		,
M26391	suppressor gene; cell cycle regulator)	A1m	2036-2296
M28489	Rsk; ribosomal protein S6 kinase	B6i	1191-1436
M29464	Pletelet- derived growth factor (A chain) (PDGF- A)	F4b	152-425
M28698	Cytoskeletal epidermal keratin (19 human)	F5j	194-500
M29475	RAG-1; V(D)J recombination activating protein	C7g	2155-2404
M29855	Interleukin-3 receptor	E3d	1975-2254
M30642	K-fibroblast growth factor	F3c	309-577
M34381	Octamer binding transcription factor (Oct 3)	D5k	774-999
M33960	Plasminogen activator inhibitor	F7h	1096-1344
M33158	CD3 antigen, delta polypeptide	E6c	73-361
M34857	Homeo Box protein 2.5 (Hox-2.5)	D4c	11-277
M36829	HSP84: heat shock 84kD protein	B1c	342-366
M55617	Mast cell protease (MMCP) - 4	F7b	634-992
M61177	Erk1; extracellular signal-regulated kinase 1; p44; Ert2	B5h	115-373
	PI3-K p85; phosphatidylinositol 3-kinase regulatory subunit;		
M60651	phosphoprotein p85; PDGF signaling pathway member	B6k	981-1260
	p58/GTA; galactosyltransferase associated protein kinase (cdc2-related		:
M58633	protein kinase)	A7b	1022-1284
M64086	Serine protease inhibitor 2 (spi-2)	F7j	1499-1754
M64429	B-Raf proto-oncogene	A3I	1651-2036
M68513	Etk1 (Mek4; HEK) tyrosine-protein kinase receptor HEK	B2I	2681-2915
M64796	RAG-2; V(D)J recombination activating protein	C7h	671-944
M84324	Collagenase type IV	F6k	696-1040
M83336	Interleukin-6 receptor beta chain; membrane glycoprotein gp130	B3c	1423-1741

TABLE 2 (CONT)

			1000 1000
	Alpha cardiac myosin heavy chain	F5e	2034-2331
	Retinoic acid receptor RXR- gamma	Def	701-1082
	Granulocyte-macrophage colony-stimulating factor receptor	E2e	904-1289
	GABA-A receptor alpha-1 submit	E5d	1251-1606
M93428	Endothelial ligand for L-selectin (GLYCAM 1)	F1:	182-541
	Integrin beta 7 subunit	E7h	2142-2423
	DNAse I	Cêc	665-871
	Cortactin; protein tyrosine kinase substrate	B7h	426-653
	Adenosine A2M2 receptor	C2g	491-735
	DNA ligase I	C5j	1678-2054
	Adenosine A1M receptor	C2f	302-673
	Non-muscle myosin light chain 3	F6b	84-370
	Cathepsin H	F6i	325-694
U06924	Stat1; signal transducer and activator of transcription	B4d	1749-2104
U09507	p21/Cip1/Waf1; cdk-inhibitor protein 1	A7e	9-403
	Cdk7; MO15; cyclin-dependent kinase 7 (homologue of Xenopus MO15		
U11822	cdk-activating kinase)	A7a	454-824
U10440	p27kip1; G1 cyclin-Cdk protein kinase inhibitor, p21-related	A7f	270-454
U10551	Gem; induced, immediate early protein; Ras family member	В7а	220-471
U12570	VHL; Von Hippel-Lindau tumor suppressor protein	A2b	885-1111
U12983	Cek 5 receptor protein tyrosine kinase ligand	F1g	1037-1287
U13705	Glutathione peroxidase (plasma protein); selenoprotein.	CII	766-1046
U14135	Integrin alpha 5 (CD51)	E7c	2170-2516
U14173	Ski proto-oncogene	A49	707-1037
U17698	Abiphilin-1 (abi-1) similar to HOXD3	D1a	351-585
U17162	BAG-1; bcl-2 binding protein with anti-cell death activity	C1e	17-334
	Shc transforming adaptor protein; Src homology 2 (SH2) protein, SHB-	,	
U15784	related	A5f	1220-1451
	MAPKK4; MAP kinase kinase 4; Jnk activating kinase 1; (JNKK1; SEK1;		
U18310	MKK4)	B6c	1380-1749
U19118	Transcription factor LRG - 21	Den	618-966
U19119	Interferon inducible protein 1	D4k	1342-1636
U19463	A20 zinc finger protein; apoptosis inhibitor	C2e	1952-2293
U19596	p18ink4; cdk4 and cdk6 inhibitor	A7c	16-284
U19799	I-kB (I-kappa B) beta	B3n	419-778

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
U24160	Dvl2; dishevelled-2 tissue polarity protein	B7i	1205-1578
1120532	Nuclear factor related to P45 NF-E2	Dsh	1429-1759
1121011	MSH2 DNA mismatch repair protein; MutS homologue 2	C7a	2150-2490
U20238	GapIII; GTPase-activating protein	B7j	328-644
U25685	Syk tyrosine-protein kinase (activated p21cdc42Hs kinase (ack))	B5d	1235-1524
	p107; RBL1; Retinoblastoma gene product-related protein p107 (cell cycle	···	
U27177	requiator)	A1j	1973-2365
U28724	PMS2 DNA mismatch repair protein; yeast PMS1 homolog 2	C7d	749-1013
U29173	Limphotoxin receptor (TNFR family)	E2g	1415-1668
U31625	BRCA1; Breast/ovarian cancer susceptibility locus 1 product	A1b	5126-5430
U33626	Pml: Murine homologue of the leukemia-associated PML gene	B4b	1667-2064
1134960	Transducin beta-2 subunit	B7e	515-834
136277	I-kB (I-kappa B) alpha chain	B3m	541-823
U37522	TRAIL; TNF-related apoptosis inducing ligand; Apo-2 ligand	C5c	981-1288
	p130; Retinoblastoma gene product-related protein Rb2/p130 (cell cycle		
662981	regulator)	A1k	970-1321
1136340	CACCC Box- binding protein BKLF	D1j	826-1065
1139643	FAF1: Fas-associated protein factor, apoptosis activator	СЗе	423-681
1141671	Zinc finger transcription factor RU49	D7m	1229-1591
1142190	GTBP: G/T-mismatch binding protein; MSH6	Ceg	1477-1769
U43144	PLC beta; phospholipase C beta 3	B6i	1933-2271
	Frizzled-3; Drosophila tissue polarity gene frizzled homologue 3;	(
U43205	dishevelled receptor	BZm	2037-7502
U43187	MAPKK3; MAP kinase kinase 3 (dual specificity) (MKK3, MEK3)	B6b	1436-1742
U43525	Myeloblastin; trypsin-chymotrypsin related serine protease	A7I	503-807
U47104	Zinc finger Kruppel type Zfp 92	D7I	578-896
U44088	TDAG51; couples TCR signaling to Fas (CD95) expression	C5a	729-1042
U43788	POU domain, class 2, associated factor 1	Dec	610-884
U48853	Cas; Crk-associated substrate; focal adhesion kinase substrate	B4I	1982-2216
U49112	ALG-2; calcium binding protein required for programmed cell death	C2i	527-861
U49739	Unconventional myosin VI	F6e	3784-4021
U51037	Transcription factor CTCF (11 zinc fingers)	Del	1625-1911
U53925	Transcription factor C 1	D6k	3895-4227

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
	Madr1; mSmad1; Mothers against dpp protein (Mad) murine homologue;		
U58992	TGF-beta signaling protein-1 (bsp-1); candidate tumor suppressor gene	A1g	238-476
U59746	Bcl-W apoptosis regulator; Bcl-2 family member	C1i	153-368
U60530	Mad related protein 2 (MADR2)	F3h	584-820
U62638	Cyclin C (G1-specific)	A6e	714-986
U63386	Mph-1 nuclear transcriptional repressor for hox genes	D5a	1621-1884
U66887	Rad50; DNA repair protein	C7f	1383-1707
U70324	Fyn proto-oncogene; Src family member	B5a	584-882
X01023	c-myc proto-oncogene protein	A2I	379-667
	c-Fos proto-oncogene; transcription factor AP-1 component. fos cellular		
V00727	oncogene	A2h	482-734
X06086	Cathepsin L	F6j	267-588
X04648	Glutamate receptor channel subunit gamma	E6n	41-408
X12616	c-Fes proto-oncogene	A41	2342-2598
X12822	Cytotoxic cell protease 2 (B10)	F6I	439-686
X07439	Homeo Box protein 3.1 (Hox-3.1)	D4d	449-722
X13721	Homeo Box protein 2.4 (Hox-2.4)	D4b	1949-2284
X14897	Fos-B; c-fos-related protein fos B	A3c	920-1278
X16490	Plasminogen activator inhibitor-2	F7i	674-978
X51983	c-ErbA oncogene; thyroid hormone receptor.	A2g	400-675
X53337	Cathepsin D	F6h	587-894
X51438	Vimentin	F6d	868-1096
X53476	HMG-14 non histone chromosomal protein	D3m	643-1017
X53798	Macrophage inflamatory protein 2 alpha (MIP 2 alpha)	F3g	14-352
X56906	Bone morphogenetic protein 7 (BMP-7) (osteogenic protein 1)	F1e	670-971
X56959	Transcription factor SP1P (POUdomain transcription factor)	D7f	866-1128
X59252	Homeo Box protein 8 (Hox-8)	D4g	826-1132
X59927	Fibroblast growth factor receptor 4	E2b	2446-2820
X57277	Rac1 murine homologue	B7c	425-651
X60831	Transcription factor UBF	D7h	689-993
X61435	Kinesin heavy chain	F5n	1898-2182
X61800	CCAAT- Binding transcription factor (C/ EBP)	D1k	904-1150
X62622	TIMP-2 tissue inhibitor of metalloproteinases-2	F7m	1236-1468
X63190	Ets-related protein PEA 3	D3a	1702-2040

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
X64361	Vav; GDP-GTP exchange factor; proto-oncogene	B7f	1083-1351
X63963	PAX-6 (paired box protein)	Deb	1081-1325
X66032	Cyclin B2 (G2/M-specific)	A6d	874-1236
	Chop10; murine homologue of Gadd153 (growth arrest and DNA-damage-		
X67083	inducible protein)	C3a	17-332
X67914	PD-1 possible cell death inducer; lg gene superfamily member	C4f	1481-1734
X69619	Inhibin beta A subunit (TGF beta family)	F2h	1064-1304
	Vegfr2; KDR/flk1 vascular endothelial growth factor tyrosine kinase		
X70842	receptor	B3j	1394-1721
X70296	Protease nexin 1 (PN-1)	F7d	746-985
X71327	MRE-binding transcription factor	D5b	552-916
X72711	Activator -1 140 KD subunit (replication factor C 140KD)	C5e	4137-4375
X72310	DP-1 (DRTF-polipeptide 1) cell cycle regulatory transcription factor	D2g	925-1305
X72230	5-Hydroxytryptamine (serotonin) receptor 1c	E4g	982-1314
X72795	Gelatinase B	F6n	599-954
X74351	XPAC; xeroderma pigmentosum group A correcting protein	C7m	447-669
X75427	Integrin alpha 2 (CD49b)	E7a	1595-1976
X77113	Growth/ diffferentiation factor 2 (GDF-2)	F2c	939-1329
X81582	Insulin-like growth factor binding protein-4 (IGFBP-4)	F2I	781-1140
X81579	Insulin-like growth factor binding protein-1 (IGFBP-1)	F2j	27-256
	IGFBP-2; insulin-like growth factor binding protein 2; autocrine and/or		
X81580	paracrine growth promoter	A5m	449-817
X81583	Insulin-like growth factor binding protein-5 (IGFBP-5)	F2m	461-824
X81584	Insulin-like growth factor binding protein -6 (IGFBP 6)	F2i	701-1039
X82327	A-myb proto-oncogene; myb-related protein A	A2e	1017-1334
X83536	Membrane type matrix matalloproteinase	F7c	877-1101
X87257	Elk-1 ets-related proto-oncogene	A3a	1498-1680
X86925	E2F-5 transcription factor	D2h	426-728
X90829	Lbx 1 transcription factor	D4n	1000-1306
X91144	P-selectin (glycoprotein ligand-1)	Esl	1095-1323
X91753	Transcription factor SEF2	D7e	755-1054
Z11974	Macrophage mannose receptor	E2h	807-1197
X95403	Rab-2 ras-related protein	B7b	232-505
X98055	Gluthathione S-transferase (theta type1); phase II conjugation enzyme	C2c	14-298
X99063	Zyxin; LIM domain protein; alpha-actinin binding protein	B7n	1437-1812

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
Y00671	Met protooncogene	A4d	3646-3933
	c-Kit proto-oncogene (mast/stem cell growth factor receptor tyrosine		
Y00864	kinase)	A4c	2867-3181
Y07960	Transcription factor BARX1 (homeodian transcription factor)	D6j	723-973
X95346	PLC gamma; phospholipase C gamma	B6m	180-516
Z12604	Stromelysin-3; matrix metalloproteinase-11 (MMP-11)	C4n	1463-1806
214224	5-Hydroxytryptamine (serotonin) receptor 1e beta	E4h	530-774
Z15119	5-Hydroxytryptamine (serotonin) receptor 2c	E4i	588-940
219521	Low density lipoprotein receptor	E4d	1047-1324
Z23107	5-Hydroxytryptamine (serotonin) receptor 7	E4k	460-817
	c-Mpl; thrombopoietin receptor; hematopoietic growth factor receptor		
Z22649	superfamily member	A5k	1561-1772
Z21848	DNA-polymerase delta catalytic subunit	Ceb	1256-1600
Z29532	Follistatin	F1I	764-1053
247766	Cyclin F (S/G2/M-specific)	A6j	2431-2708
Z36885	Ets-related protein Sap 1A	D3c	1267-1521
Z32815	Net; ets related transcription factor; activated by Ras	A3i	1211-1595
Z48538	Stat5a; mammary gland factor	B4f	2269-2628
	Hek2 murine homologue; Mdk5 mouse developmental kinase; Eph -related		
Z49086	tyrosine-protein kinase receptor	B2n	1702-1930
D26177	D-Factor/LIF receptor	딢	2376-2775
M13806	Cytoskeletal epidermal keratin (14 human)	F5h	108-469
M21019	R-ras protein, closely related to ras proto-oncogenes	B7d	215-555
M22959	Prolactin receptor PRLR2	E4c	1-328
M30903	Blk; B lymphocyte kinase; Src family member	CZj	1307-1672
M35590	Macrophage inflamatory protein 1 beta (Act 2)	F3f	119-445
M75716	Alpha-1 protease inhibitor 2	F7g	625-969
M92378	GABA-A transporter 1	E5e	1131-1416
M97017	Bone morphogenetic protein 8a (BMP-8a) (TGF-beta family)	F1f	788-1139
M97200	Erythroid kruppel-like transcription factor	D2n	783-1171
M98339	GATA binding transcription factor (GATA-4)	D3e	81-379
M98547	Growth factor receptor	E2f	1701-2014
S72408	Crk adaptor protein	B4m	750-1027
U09419	Retinoid X receptor interacting protein (RIP 15)	D6g	1388-1682
U14752	Cek 7 receptor protein tyrosine kinase ligand	F1h	504-837

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
	C-C CKR-1; CCR-1; C-C chemokine receptor type 1, macrophage		460 406
U29678	Inflammatory protein-1 alpha receptor; MIP-1alpha-H; HAN1ES-H	971	108-435
X13358	Glucocorticoid receptor form A	E3m	1527-1816
	Mothers against DPP protein (mad homolog Smad 1, transforming growth		
X83106	factor beta signaling protein)	F3j	464-728
Y00487	Hck tyrosine-protein kinase	B5b	1308-1563
AB000777	Photolyase/blue-light receptor homologue	C7c	1418-1737
D49482	Osp94 osmotic stress protein; APG-1; hsp70-related	B1f	1026-1266
D78645	Glucose regulated protein, 78kD; Grp78	B1m	167-411
	LCR-1; CXCR-4; CXC (SDF-1) chemokine receptor 4; HIV coreceptor		
D87747	(fusin); G protein-coupled receptor LCR1 homologue;	B3d	584-867
M23384	Glucose transporter-1, erythrocyte; Glut1	B2e	325-653
M80456	Int-3 proto-oncogene; NOTCH family member; NOTCH4	A5h	1846-2145
M94335	c-Akt proto-oncogene; Rac-alpha; proteine kinase B (PKB)	C2k	604-899
Y13231	Bak apoptosis regulator; Bcl-2 family member	C1f	1509-1786
U57324	PS-2; homologue of the Alzheimer's disease gene	C4h	437-783
U65594	BRCA2; Breast cancer susceptibility locus 2 product	A1c	649-922
U66058	DNA ligase III	C5k	2980-3205
U67321	Caspase-7; Lice2; ICE-LAP3 cysteine protease	C1c	1040-1280
U75506	BID; apoptic death agonist	C1k	452-777
	WBP6; pSK-SRPK1; WW domain binding protein 6 serine kinase for SR		
U92456	splicing factors	B7m	482-774
U95826	Cyclin G2 (G2/M-specific)	A6l	408-688
X99018	Ung 1; uracil-DNA glycosylase	C7I	444-729
Y14019	Rab-3b ras-related protein	F6c	232-562
U28423	Inhibitor of the RNA-activated protein kinase, 58-kDa	B5i	180-487
U34259	Golgi 4-transmembrane spanning transporter; MTP	B2d	742-1060
U34920	ATP-binding casette 8; ABC8; homolog of Drosophila white	B2b	1011-1319
U37720	CDC42 GTP-binding protein; G25K	F5g	1675-1982
U41751	Etoposide induced p53 responsive (EI24) mRNA	B11	1041-1296
U51866	Casein kinase II (alpha subunit)	A3n	1237-1517
U52945	TSG101 tumor susceptibility protein	A1n	446-713
U54705	Turnor suppressor maspin	A2a	251-507
92076	FLIP-L; apoptosis inhibitor; FLICE-like inhibitory protein	C3h	1476-1811
X63615	CamK II; Ca2+/calmodulin-dependent protein kinase II (beta subunit)	F5f	1951-2219

TABLE 2 (CONT)

		A zeros Coordinoto	Docition
GenBank #	Gene Name	Ailay cooluliate	T CONTROLL
	Htk; Mdk2 mouse developmental kinase; Eph -related tyrosine-protein	i	4
Z49085	kinase receptor	B3a	2032-2365
D49921	Glial cell line-derived neurotrophic factor	F1n	236-539
L06039	CD31 (Platelet endothelial cell adhesion molecule 1)	E6d	1172-1494
116928	CD22 antigen	E6i	2314-2645
L39770	Gbx 2	D3g	1122-1395
M12302	Cytotoxic T lymphocyte-specific serine protease CCP I gene (CTLA-1)	F6m	585-830
M14222	Cathepsin B	F6g	382-729
M33324	Growth hormone receptor	E3n	1942-2240
M34563	CD28 (receptor for B71)	E6b	544-774
M38651	Estrogen receptor	E3I	742-1013
S71251	Monotype chemoattractant protein 3	E1k	201-491
U03856	CD45 associated protein (CD 45-ap, LSM-1)	E6f	620-898
U11688	Orphan receptor	E1b	1686-1943
117985	Cannabinoid receptor 1 (brain)	E4n	1091-1437
U43512	Dystroglycan 1	E6m	2267-2505
1146923	G-protein coupled receptor	E5c	350-671
X02389	Urokinase type plasminogen activator	F7f	1301-1538
X05719	CTLA-4 (immunoqlobin superfamily member)	E6k	246-519
X56182	Myogenic factor 5	D2d	232-528
X62700	uPAR1: urokinase plasminogen activator surface receptor (CD87)	B3i	482-756
X69832	Serine protease inhibitor 2.4	F7k	621-927
X70298	SRY-box containing gene 4	D7b	34-311
125602	Bone morphogenetic protein 2 (BMP-2) (TGF-beta family)	F1c	8372-8724
M10021 [KO:	M10021 [K024[K02588] P-1-450; dioxin-inducible cytochrome P450	B2a	3729-4014
M16506	Bct-2; B cell lymphoma protein 2, apoptosis inhibitor	Cth	2125-2367
M34510	CD14 antigen	E6h	667-931
M81832	Somatostatin receptor 2	E3b	47-310
U19880	Dopamine receptor 4	E5b	907-1191
U21681	Cannabinoid receptor 2 (macrophage, CB2)	E5a	910-1262
U58533	Erf (Ets-related transcription factor)	D2m	1286-1613
211597	5-Hydroxytryptamine (serotonin) receptor 1b	E4f	1043-1355
D78382	Tob antiproliferative factor; interacts with p185erbB2	A7n	540-876
J03752	Glutathione S-transferase (microsomal)	C2a	185-428
L20331	Adenosine A3 receptor	C2h	182-382

TABLE 2 (CONT)

GenBank #	Gene Name	Array Coordinate	Position
U05341	p55cdc; cell division control protein 20	C4e	1061-1348
U12273	AP endonuclease; apurinic/apyrimidinic endonuclease (Apex)	CSf	1894-2150
X67735	Mas proto-oncogene (G-protein coupled receptor)	A5I	566-808
D26046	AT motif-binding factor ATBF1	D1d	9807-10112
D49474	HMG-box transcription factor from testis (MusSox17)	D3I	427-662
L03547	Ikaros DNA binding protein	D4i	627-890
L12147	Early B cell factor (EBF)	D2a	750-1026
L12703	Engrailed protein (En-1) homolog	D2b	1323-1554
L12705	Engrailed protein (En-2) homolog	D2c	1626-1895
L21027	Transcription factor A10	B4i	499-806
L26507	Myocyte nuclear factor (MNF)	D5c	1203-1456
L36435	Basic domain/leucine zipper transcription factor	D1e	872-1073
M37163	Caudal type Homeobox 1 (Cdx1)	D1I	1040-1301
M58566	Butyrate response factor 1	D1i	768-1054
S53744	Brain specific transcription factor NURR-1	D1g	1548-1754
S68377	Brn-3.2 POU transcription factor	D1h	877-1237
S74520	Caudal type Homeobox 2 (Cdx2)	D1m	1085-1367
U01036	Erythroid transcription factor NF-E2	D2d	1-241
U20344	Gut-specific Kruppel-like factor GKLF	D3i	1558-1789
U25096	Kruppel-like factor LKLF	D4m	898-1193
U29086	Neuronal helix-loop-helix protein NEX-1	D5e	572-907
U36760	Brain factor 1 (Hfhbf1)	D1f	1080-1318
U41626	Split hand/foot gene	D5m	92-303
U42554	Sim transcription factor	D1n	2828-3066
U59876	Glial cells missing gene homolog (mGCM1)	D3h	727-1080
U62522	Sp4 zinc finger transcription factor	D4j	1704-1929
X61754	Heat shock transcription factor 2 (HSF 2)	D3j	1445-1640
X83974	RNA polymerase I termination factor TTF-1	A2j	3222-3433
L35949	Hepatocyte nuclear factor 3/forkhead homolog 8 (HFH-8)	D3k	913-1232
X94125	SRY-box containing gene 3 (Sox3)	D5n	212-443
D13759	Cot proto-oncogene	A3m	696-956
	HR21spA; protein involved in DNA double-strand break repair; PW29;		
D49429	calcium-binding protein	Ceh	103-434
707407	MmLim15; RecA-like gene; DMC1 homologue; meiosis-specific	<u>19</u>	504 704
1004107	Homologous recombination protein	<u></u>	10/-100

TABLE 2 (CONT)

		Array Coordinate	Docition
GenBank #	Gene Name	Allay Cooldinate	100100
	ERp72 endoplasmic reticulum stress protein; protein disulfide isomerase-	-	4460 4470
J05186	related protein	БТК	1150-1470
\$50213	HMG1-related VDJ recombination signal binding protein	B1h	2263-2531
S65038	Gli oncorene: zinc finger transcription factor	A3e	104-505
105245	Tram-1 invasion inducing protein; GDP-GTP exchanger-related	A5n	4329-4628
1116805	Sik-Src-related intestinal kinase	C4k	1246-1623
1128405	I fo proto-oncodene	A5d	853-1150
020433	Oxidative stress-induced protein mRNA	B1n	1248-1561
1143900	STAM: signal transducing adaptor molecule	C4m	576-811
043300	Short adaptor: Sho-related: brain-specific	C7i	246-601
1158987	MmMre11a putative endo/exonuclease	B1i	866-1204
VESOGS	PCNA: proliferation cell nuclear antigen; processivity factor	C7b	53-320
A33000	Translin recombination hotspot binding protein	C7j	205-431
X056404	DA6 stromal protein: BAG1 nene activator	C6a	442-749
A90010	Sky proto-pacogene (Tvro3: Bse: Dtk)	A4h	1927-2286
750042	Li ras proto-oncodene transforming G-protein	A5c	1307-1544
250013	EBBB-2 recentor (c-nell HER2 protein tvrosine kinase)	E1m	16-42
147240	EBBB-3 recentor	E1n	4-243
1122516	Placental ribonuclease inhibitor (Angiogenin)	F4a	512-766
025310	myosin I	G13	2578-2921
11459777	Ca2+ hinding protein. Cab45	G20	597-1082
M10624	murine ornithine decarboxylase	G14	865-1252
W110064	ithionitin	G5	123-547
A31703	Hypovantine-guanine phosphoribosyltransferase	25	301-751
200423	Trypoxamino gamino processione 2	G6	446-813
07,0047	ribosomal protein \$29	G21	5-244
1003	Akveraldehvde-3-nhosnhate dehvdrogenase	G12	765-1016
W323939	Universities of productions and a second production of the continuous continu	G19	25-564
M12481	Dela-aciili		

Cancer Array

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In the cancer arrays of the subject invention, the polynucleotide probe compositions on the array correspond to those genes which are associated, e.g. play a role in, cellular proliferative diseases, particularly cancer, where human genes are of particular interest in many embodiments. Types of genes that are typically represented on a cancer array of the subject invention include: oncogenes, tumor suppressors, cell cycle regulators, genome plasticity genes, apoptosis genes, cell differentiation genes, regulators of tumor host interaction and metastasis, such as extracellular matrix proteins, cell adhesion receptors, molecules that control cell invasion and motility, and genes associated with angiogenesis.

In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: cell cycle/growth regulators; apoptosis; growth factors/cytokines; oncogenes/tumor suppressors; cell adhesion, motility and invasion; invasion regulators; GTP ases and their regulators; cadherins; intermediate filament markers; receptors; cell fate/development regulators; DNA damage/response/repair/ recombination; and angiogenesis regulators. In a specific cancer array of interest, the spots are as listed in Table 3.

The cancer array finds use in a variety of applications, including: monitoring cellular responses to therapeutic compounds; comparing expression profiles of tumors at different developmental stages; developing diagnostic tools for distinguishing closely related tumors; and the like.

In the following Table 3, as well as preceding Tables 1 and 2, the "position" coordinate refers to the actual nucleotide residues of the listed gene that are represented on the array.

TABLE 3

	7	Array Coordinate	Docition
Cell Cycle/Growth Regulators	Genbank #	Allay Cooldinate	
QUADRANT A			
CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1) (P34 DEDATEIN KINASE) (CYC. IN-DEPENDENT KINASE 1) (CDK1)	X05360	A1a	655-886
CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1) (P33 PROTEIN	M68520	A1b	1774-2180
CELL DIVISION DROTEIN KINASE 3 (EC 2.7.1-)	X66357	A1c	216-882
CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1) (PSK-J3)	M14505	A1d	372-693
CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1) (TAU PROTEIN	X66364		
(KINASE PSSALRE).		A1e	468-767
CFIT DIVISION PROTEIN KINASE 6 (EC 2.7.1) (KINASE PLSTIRE)	X66365	Ali	313-003
CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1) (CDK-ACTIVATING KINASE) (CAK) (39 KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1).	L20320	Ala	89-305
CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P391	U34051	8 4 k	763.1.69
PRECURSOR (CDK5 ACTIVATOR) (P39I).		AIN	703-1-02
CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR) (TAIL PROTEIN KINASE II 23 KD SUBUNIT) (TPKII	X80343		
DECLINATION (1701 171 (1702) (1707) (1707)		A1i	551-941
CACOSA M. PHASE INDITCER PHOSPHATASE 1 (EC 3.1.3.48)	M81933	A1j	1632-1978
cdc25B; M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48).	M81934; [S78187]		0000
(CDC25Hu2)		AIK	2002-0022
odc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).	M34065	A11	331-623
CIK-1	L29222	A1m	144-459
CIK-2	L29216	A1n	1106-1356
CI K-3	L29220	A2a	551-1002
SERINE/THREONINE-PROTEIN KINASE KKIALRE	X66358	A2b	276-461
SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	X66363	A2c	1114-1434
SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2	X66360	A2d	954-1250
SERINE/THREONINE PROTEIN KINASE PCTAIRE-3	X66362	A2e	549-911
SERINE/THREONINE PROTEIN KINASE PITALRE	L25676	A2f	367-635
	M80629	A2g	1388-1548
CDC2-RFI ATED KINASE PISSLRE	L33264	A2h	454-755
	X51688	A2i	876-1218
CYCLIN B1 G2/MITOTIC-SPECIFIC	M25753	A2j	979-1311
CYCLIN C G1/S-SPECIFIC	M74091	A2k	6670-7326
CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE)	X59798; [M64349]	A2I	3427-3784
	D13639 [M90813]	A2m	3932-4284
CYCLIN D3	M92287	A2n	537-894

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	GenBank #	Array Coordinate	Position
CYCLINE	M73812	A3a	
CYCLIN G1	U47413 [L49504]	A3b	755-1035
CYCLIN G2	U47414 [L49506]	A3c	989-1254
CYCLIN H	U11791 [U12685]	A3d	717-1026
CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA	U09579; [L25610]		
DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (MAE1) (CDKN14) (CDKN14)			
(PIC1) (CAP20)		A3e	1745-2063
CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITO	U22398	70 4	0.00
CYCLIN-DEPENDENT KINASE 4 INHIBITOB A (CDK4!) (P16-INK4) (P16-	1 27211	100	1040-1310
INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). (CDKN2A)		A3g	482-836
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) U17075; [L36844]	U17075; [L36844]		
(MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B).		A3h	116-462
CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).	U40343; [U20498]	A3i	750-952
WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112) (Wee1Hu)	U10564	(A3j	1259-1502
SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1) (PLK-1)	U01038		
		A3k	1330-3233
PHOSPHOLIPASE D1	U38545	A3i	2862-3961
NEDDS PROTEIN HOMOLOG.	D63878	A3m	381-675
CDC10 PROTEIN HOMOLOG	S72008	A3n	628-99
CDC27HS PROTEIN	U00001	A4a	870-3474
UBIQUITIN-CONJUGATING ENZYME E2-CDC34	L22005	A4b	249-550
CDC16HS.	U18291	A4c	45-378
CDC37 HOMOLOG.	U63131	A4d	519-1464
	U77949	A4e	216-447
	X60188		
(INSULIN-STIMULATED MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44 FR12) (P44-MAPK) (MICROTI IRII FASSOCIATED PROTEIN 2			
KINASE).		A4f	754-1094
EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1) (ERK3)	X80692		
		A4g	806-1267
INASE 4 (EC 2.7.1) (ERK4)	X59727		
(MAP KINASE ISOFORM P63) (P63-MAPK).		A4h	2678-2994
EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1) (ERK5) (FRK4) (BMK1 KINASE)	U25278		1010 1067
SIGNAL-REGULATED KINASE 6 (EC 2.7.1) (ERK6)	X79483		1010-1507
		A4j	530-831

TABLE 3 (CONT)

			Decition
Cell Cycle/Growth Regulators	Genbank #	Array Coordinate	LOSINO
MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1) (MAP	L35253; [L35263]		
BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-		, i	7007
INTERACTING PROTEIN 2) (MAP KINASE MXI2).		A4K	925-1204
STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1) (C-JUN N-	L26318	241	952-1263
TERMINAL KINASE 1) (JNK-46)		1.4	205-1500
STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1) (C-JUN N-	L31951		4000
TERMINAL KINASE 2) (JNK-55).		A4m	638-1000
STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1) (C-JUN N-	U34819; [U07620]		
TERMINAL KINASE 3) (JNK3) (MAP KINASE P49 3F12).		A4n	1018-1413
DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE	U25265		
5 (EC 2.7.1) (MAP KINASE KINASE 5) (MAPKK 5) (MAPK/EHK KINASE		45.9	629-847
5).		ASA	10.030
DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE	L05624		
1 (EC.2./.1) (MAP KINASE KINASE I) (WATKN 1) (EDIN ACTIVATION II)	-	A5b	842-1217
KINASE I) (WATIVEDIK KINASE I) (MEKI).	1120657		
DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN NINASE NINASE	100800		
6 (EC. 2.7.1) (MAP NIVAGE NIVAGE O) (MAP NA O) (MAI 19 E) WATER		A5c	1060-1389
MEK KINASE 3	U78876	A5d	1195-1453
PONA (CYCLIN)	M15796; [J04718]	A5e	157-436
pini	U49070	ASf	624-1075
BBD1/BETINORI ASTOMA-BINDING PROTEIN)	S57153; S57160	A5g	2676-2889
ESE. 1 oBB-hinding protein	M96577	A5h	899-1595
F5F-3	Y10479	A5i	698-897
F2F-5	U15642	A5j	645-922
F2F-related transcription factor (DP-1)	L23959	A5k	935-1186
DP2 (Humdp2), dimerization partner of E2F	U18422	A5I	1603-1838
RBO-3	X85134	A5m	359-603
GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1).	L13698	A5n	1550-1701
growth inhibitor p33ING1 (ING1)	AF001954	A6a	722-983
Abl interactor 2 (Abi-2) + Abl binding protein 3 (AbIBP3) [ArgBPIB]	U23435; U31089	A6b	1049-1203
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTOR	L29511; [M96995]		
PROTEIN) (ASH PROTEIN).		A6c	355-573
GRB-IR / GRB10	U69276	A6d	358-1155
RAF ONCOGENE	X03484	A6e	1704-1989
-d'jer	M95712	A6f	866-1144
jun B TRANSACTIVATOR	M29039	A6g	1197-1442
N-mγc	M13228	A6h	761-1188

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	GenBank #	Array Coordinate	Position
C-myc binding protein	D89667	A6i	218-490
INTERMEDIATE FILAMENT MARKERS			
SYTOKERATIN 9) (K9) (CK 9).	Z29074; [S69510]	A6j	652-1781
TOSKELETAL 10 (CYTOKERATIN 10) (K10) (CK	M19156	A6k	295-497
PATIN, TYPE I CYTOSKELETAL 12 (CYTOKERATIN 12) (K12)	D78367	A6I	455-624
	X52426; X07696; X62571		
13) +KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15)			
(CN 13) +NEDA1114, 117 E 1 C11 CONCEELTAE 17 (C11 C11 C11 C11 C11 C11 C11 C11 C11 C1		A6m	383-1001
KERÁTIN, TÝPE I CYTOSKELETAL 14 (CYTOKERATIN 14)(K14) (CK 14) J00124	J00124	A6n	339-839
KERATIN, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16)(K16) (CK	M21772; M20336		
16);pseudo-keratin K16 type I		A7a	32-522
KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 18)	M26326	A7b	706-971
KÉRATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).	Y00503	A7c	726-1124
KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (K1) (CK 1) (67 M98776 KD CYTOKERATIN) (HAIR ALPHA PROTEIN)	M98776	A7d	894-1459
CYTOKERATIN 2P) (K2P)	М99063	A7e	2167-2455
KERATIN, TYPE II CYTOSKELETAL 2 EPIDERMAL (CYTOKERATIN 2E) (KZE) (CK 2E)	M99061 [S43646]	A7f	1091-1450
KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)	X67683	A7g	66-404
KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 M21389 KD CYTOKERATIN)	M21389	A7h	93-682
KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) + (CYTOKERATIN 6B) (CK 6B) (K6B KERATIN) + (CYTOKERATIN 6C) (K6C KERATIN) + (CYTOKERATIN 6D)	J00269; V01516; L42592; L00205; L42601; L42610; L42611: L42612		
(CK 6D) (K6D KERATIN) + (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN)	1	A7i	689-880
KERATIN, TYPE II CYTOSKELETAL 6B (CYTOKERATIN 6B) (CK 6B)	L42592; L00205	A7i	275-414
KERATIN, TYPE II CYTOSKELETAL 7 (CYTOKERATIN 7) (K7) (CK 7)	X03212	A7k	1154-1430
KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8) (CK 8)	M34225	A7I	1190-1474
VIMENTIN	X56134 [M14144]	A7m	460-740
DESMIN	U59167	A7n	1063-1364

TABLE 3 (CONT)

Domilotore	GenBank #	Array Coordinate Position	Position
ANT B			
APOPTOSIS			
	M14745	Bla	5078-5382
nd n53 hinding protein Bbp/53BP2 (BBP/53BP2)	U58334		3129-3376
	L22474	B1c	227-478
PTOSIS REGIII ATOR BCL-W	U59747	B1d	121-403
LEUKEMIA CELL DIFFERENTIATION PROTEIN	L08246		100
		B1e	//6-/69
DIETIC-	U29680		000
		811	64-293
() (BP4)	X89986; [U34584]	310	935-1200
(BIP1) (BIK)	1123765- [1116812-		
BCL-2 HOMOLOGOOD ANTAGONISTINELETT (72 CT. 100)	\sim	B1h	1371-1661
DAN DEOTEIN (RC) -2 RINDING COMPONENT 6).	U66879	B1i	408-749
RCI -2 BINDING ATHANOGENE-1 (BAG-1) (GLUCOCORTICOID	S83171; [Z35491]		
RECEDIOR-ASSOCIATED PROTEIN RAP46).		B1j	511-830
serioe/threonine protein kinase NIK: binds specifically to TRAF2	Y10256	B1k	3776-4036
3H-alpha+	AF010127[Y14039;		
	Y14040]	B1I	363-787
daptor molecule for	U84388		
caspase-2 and FasL/TNF receptor-interacting protein RIP		B1m	369-604
TNF recentor-1 associated protein (TRADD)	L41690	B1n	1009-1313
cell death protein kinase BIP	U25994; [U50062]	B2a	848-1123
DAXX a FAS-hinding profesh that activates JNK and apoptosis	AF015956	B2b	804-1030
Ano2 linand (TNF-related apoptosis inducing ligand TRAIL)	U57059	B2c	211-616
TRAF-INTERACTING PROTEIN I-TRAF (TRAF family member-associated U59863; [U63830]	U59863; [U63830]	703	674-887
NF-KB activator LAINA	1169108	B2e	1318-1694
IMATS	1178798· [1 81153]	B2f	1689-1961
LHAFD TOUR	1177845	B2a	154-387
HAR-interacting protein (Thir)	U12597	BZh	1207-1566
CD40 RECEPTOR ASSOCIATED FACTOR 1 (CRAF1) (CAP-1), (LMP1	U21092; [U15637; L38509;	;ca	080 1300
associated protein)	U1926U	פלו	300-1366
INHIBITOR OF APOPTOSIS PROTEIN 1 (HIAP1) (HIAP-1) (C-IAP2)	 U45878; [U37546]		
(IM IZ-IIIA) O'CHANA (COM ZENTA (-	B2j	1444-1848

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	GenBank #	Array Coordinate Position	Position
INHIBITOR OF APOPTOSIS PROTEIN 2 (HIAP2) (HIAP-2) (C-IAP1) (TNFR2- TRAF SIGNALLING COMPLEX PROTEIN 2) (IAP HOMOLOG B)	U45879; [U37547]		
(IAP2) (MIHB).		B2k	266-621
HIBITOR OF APOPTOSIS PROTEIN (X-LINKED IAP) (IAP-	U45880; [U32974]		
LIKEPROTEIN) (HILP).			2000-2363
with regulator CGR19	U66469		28-301
cytotoxic ligand TRAIL receptor	U90875	B2n	290-548
(ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-U13699; [M87507; X65019]	U13699; [M87507; X65019]		
		ВЗа	5078-5282
	U13021; [U13022]	B3b	851-1218
	U13737		
(YAMA PROTEIN) (CASPASE-3) (CPP32) (YAMA PROTEIN) (CASPASE-		Č	7070
3) isotorm alpha		B3C	2007-2434
ICH-2 PROTEASE PRECURSOR (EC 3.4.22) (TX PROTEASE) (ICEREL-U28014; U28015	U28014; U28015		
II) (CASPASE-4) + CASPASE-5 PHECORSOR (EC 3.4.22) (ICH-3			
PROTEASE) (TY PROTEASE (ICEREL-III).		B3d	763-11-07
CASPASE-6 PRECURSOR (EC 3.4.22) (APOPTOTIC PROTEASE MCH- U20537; U20536	U20537; U20536		
2) isoform beta + isoform alpha		ВЗе	387-697
CASPASE-7 PRECURSOR (EC 3.4.22) (ICE-LIKE APOPTOTIC	U37448		
PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1)			
		B3f	1042-1413
ISOR (EC 3.4.22) (ICE-LIKE APOPTOTIC	U60520; U58143; X98172;		
PROTEASE 5) (MORT1-ASSOCIATED CED-3 HOMOLOG) (MACH)	X98173; X98174; AF00962		
(FADD-HOMOLOGOUS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE)			
(FLICE) (APOPTOTIC CYSTEINE PROTEASE) (APOPTOTIC			
PROTEASE MCH-5) (CAP4) (CASP8) (MCH5) isof		B3g	1327-1607
	U60520; U58143; X98172;		
1-ASSOCIATED CED-3 HOMOLOG) (MACH)	X98173; X98174;		
IS ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE)	AF00962;X98176; X98175;		
<i>r</i> ¬	X98177; X98178		
PROTEASE MCH-5) (CAPP4) (CASP8) (MCH5) isof		B3h	475-954
CASPASE-9 PRECURSOR (EC 3.4.22) (ICE-LIKE APOPTOTIC	U56390; [U60521]		
PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6)		B3i	986-1289
ICE-LIKE APOPTOTIC PROTEASE 4 PRECURSOR (EC 3.4.22)	U60519		
SASE MCH-4) (CASPASE-10)		B3j	2276-2690
TED PROTEIN 3 (DAP-3) (ionizing radiation resistance	U18321; [X83544]		
conferring protein)		жж	856-1114
DEATH-ASSOCIALED PHOLEIN KINASE 1 (EC 2.7.1) (DAP KINASE 1). X76104	X76104	B3I	1988-2321

TABLE 3 (CONT)

	ConBont #	Array Coordinate Position	Position
	# 4	Ariay Cool alliance	066 1990
Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1		B3m	6021-000
	S78085	B3n	406-694
FAS/APO 1	270519	B4a	1493-1887
FASTITICEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL)	D38122; [U08137]	B4b	1400-1782
WSL-LR, WSL-S1, WSL-S2 + TRAMP (Apo-3) (DDR3)	Y09392; [U75380;U74611; U83597]	B4c	1407-1671
AM1 (rac protein kinase alpha protein kinase B. c-Akt)	M63167	B4d	
AKTO (rac protein kinase beta)	M77198; [M95936]	B4e	1867-2099
TAIL alpha converting enzyme	U69611	B4f	1540-1746
	AF016268	B4g	273-552
DOAC 1-brain-ralated anontosis gene/RCI-2 homolog	S82185	B4h	351-995
	U63295	B4i	239-523
Sevel III abserina nomong	U37688	B4j	1247-1367
TAIS! TAIA framentation factor 45	U91985	B4k	485-1592
privating anothers related protein 1	AF017986	B4I	189-974
societed approach selected profess (SABP3)	AF017988	B4m	702-841
secreted appropriate February (FAR15)	AF022385	B4n	365-520
calmodulin denendent phosphodiesterase PDE1B1	U56976	B5a	414-549
olintathione. S. transferase homolog	U90313	BSb	97-837
CD97RD (Siva)	U82938	B5c	406-625
chromosome segretation dene homolog CAS	U33286	B5d	674-1247
anonhoris inhibitor survivin	U75285	B5e	386-720
application of the second of t	AF010310 AF010311	B5f	29-771
pina (PIG3)	AF010309	B5g	398-1223
(pid) (pid)	AF010312	B5h	173-322
Pia10 (PIG10)	AF010314	B5i	437-1623
Pig13 (PiG11)	AF010315	B5j	748-1304
(pig19)	AF010316	B5k	97-531
(GTP-binding protein (rhoA)	L25080	BSI	290-572
7	M35543; [M57298]	B5m	321-468
ONCOGENES/TUMOR SUPPRESSORS			
C.EMS PROTO ONCOGENE	X03663	B5n	2568-2880
Clos	K00650	B6a	2949-3181
Cikit	X06182	Beb	1981-2375
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112)	HT2291; [K03214; X03996]	B6c	893-1189
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) M19722	M19722	B6d	521-856
(roo-ran) (c-ran).			

TABLE 3 (CONT)

	# /10000	Array Coordinate	Position
Cell Cycle/Growth Regulators	Genbank #	Allay Cooldinate	1001100
INNA MISMATCH REPAIR PROTEIN MSH2	U04045; [L47583]	B6e	1496-2178
(mutS - ALPHA 160 KD	U54777		
SUBONII) (G/I MISMAICH BINDING PROTEIN) (G.D.) (G.I)		B6f	591-1100
K-RAS ONCOGENE	M54968	B6g	352-604
	J02958	B6h	932-1242
	M14694; [M14695]	B6i	690-964
SAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN	U43746	B6j	10056-10346
	U76638	B6k	1493-1801
MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB:	Z12020; [M92424]	BAI	920-1232
U33199) + MDM2-C (GB: U33201)	AF007111	B6m	405-681
MDMC-line poor line in process of n53-related protein	Y11416	B6n	627-993
	X74594	B7a	951-1213
DBA/A40	X74262	B7b	605-974
RRPO sational stoms hinding protein	S66431	B7c	2339-2642
hinding protein	X85133	B7d	1701-1930
TYROSINE-PROTEIN KINASE RECEPTOR RET	M31213; [M57464]		
PRECURSOR (EC 2.7.1.112) (C-RET). Papillary thyroid carcinoma-		B7e	2285-2631
Botinoblastoma susceptibility (BB1 retinoblastoma-assoc)	M15400	B7f	2839-3101
CKY (DTK) (TYRO3) (RSE)	D17517	B7g	2132-2597
	M15990	B7h	1325-1676
DSINE-PROTEIN	U10087 X58957		
TYROSINE KINASE)(AGAMMAGLOBULINAEMIA 17HOSINE NINASE) IATK) (A CFL) PROGENITOR KINASE) (BPK) (BTK) (AGMX1)		B7i	380-1430
TYROSINE-PROTEIN KINASE ABL2 (EC 2.7.1.112) (TYROSINE KINASE	M35296	B7j	493-1656
TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KD ZETA- ASSOCIATED PROTEIN) (ZAP70)	L05148	B7k	1-584
	M97935		
P91/P84) (STAT1)		871	638-1376
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2 (P.113) (STAT2)	U18671 M97934	B7m	1105-1480
SIGNAL TRANSDUCER AND TRANSCRIPTION ACTIVATOR 5B (STAT5B)	U47686	B7n	831-1135
QUADRANT C			

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	GenBank #	Array Coordinate Position	Position
ONSE/REPAIR/RECOMBINATION			
A DEPENDENT	U35835; [U47077]		
PROTEIN KINASE CATALYTIC SUBUNIT (DNA-PRES) (ARCC.)		C1a	2250-2680
ATAXIA TELANGIECTASIA (ATM)	U33841	C1b	8938-9135
SSOCIATED PROTEIN (FRAP)	L34075	C1c	6750-7088
IT (LUPUS KU	M32865; [S38729]		
AUTOANTIGEN PROTEIN P70) (70 KD SUBUNIT OF KU ANTIGEN)	<u>.</u>		
(THYROID-LUPUS AUTO-ANTIGEN) (TLAA) (KU70) (CTC BOX BINDING			
_		C1d	1729-1974
(LUPUS KU	M30938		
AUTOANTIGEN PROTEIN P86) (86 KD SUBUNII OF KU ANTIGEN)			
(LINTHOID-LOPUS AUTOBINITION) (TEXX) (CTO BOX BINDING INC. INC. INC. INC. INC. INC. INC. INC.			
(KIIBO) (XBCCS)		C1e	2340-2764
IDNA EXCISION REPAIR PROTEIN ERCC1	M13194	C1f	625-938
OTIDE SYNTHASE (ATP))	X84740		
(DNL3)		C1g	2460-2780
DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))	X83441	-	1500 5050
		nio	2/8/-30/4
JLYMERASE ALPHA	X06745	C1i	3721-4093
DNA REPAIR PROTEIN RAD50	U63139	CI)	5117-5435
DNA REPAIR PROTEIN RAD51 HOMOLOG [Replication protein A (E coli	D13804	;	1
RecA homolog, RAD51 homolog)]		C1k	867-1159
DNA REPAIR PROTEIN RAD52 HOMOLOG	U12134	5	1528-1733
DNA TOPOISOMERASE I	J03250	C1m	2388-2796
DNA TOPOISOMERASE II ALPHA ISOZYME	J04088	C1n	2459-2883
DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA M31899	M31899		
PIGMENTOSUM GROUP B COMPLEMENTING PROTEIN) (DNA			
EXCISION REPAIR PROTEIN ERCCS) (BASAL TRANSCRIPTION			
		C2a	2109-2466
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA X52221; [HT1175]	X52221; [HT1175]		
FIGWEIN LOSOM GROOF D'OOM! ELMENT ING THOUGHT, (CITA)		C2b	1520-1821
INA-REPAIR PROTEIN XRCC1	M36089	C2c	1226-1539
DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA L20046; [X69978]	L20046; [X69978]		
EXCISION REPAIR PROTEIN ERCC-5)		C2d	1374-1638

TABLE 3 (CONT)

Out On the Demily of the	Gen Bank #	Array Coordinate	Position
CEIL CYCIE/GLOWIII NEGUIACOIS GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN	S40706 [S62138]		
		C2e	480-789
GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 M60974 (IDNA-DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1).	M60974	C2f	526-886
RANSFERASE (6-	M29971	C2g	241-546
MUSCLE-SPECIFIC DNASE I-LIKE [DNase X] (XIB)	X90392; [L40817; U06846]	C2h	2038-2427
DNA MICMATCH REPAIR PROTFIN MI H1 (mut. HOMOLOG)	U07418	CZi	1765-2020
	L24564	C2j	489-780
VATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD INIT) (REC36)	L07540	C2k	708-1051
ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT)	M87339	C2I	98-355
ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (REC38)	L07541	C2m	438-762
ΙŻ	M87338	C2n	882-1286
REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE STRANDED DNA-	M63488	ç	1498-1838
BINDING PROTEIN)	HT3218 [K00065]	3	198-496
SUPERIORIDE DISMOTASE (SUPERIORING ASSETTING TO TECHNICAL PHA	M96684	C3c	563-855
HHR6A (YEAST RADE HOMOLOG) (UBIQITIN-CONJUGATING	M74524	C3d	175-433
UV EXCISION REPAIR PROTEIN PROTEIN RAD23 [xeroderma pigmentosum group C repair complementing protein HHR23A]	D21235	СЗе	355-632
CELL FATE/DEVELOPMENT REGULATORS			
-Notch pathway	M73980	C3f	2701-2965
Notich 1	U77493	C3g	373-658
notch prouin protein (N)	M99437	C3h	647-1210
	U95299	C3i	3014-3169
January 1	AF028593	C3j	3884-4117
Jacobed 2	AF003521	C3k	1027-1241
DELTA-LIKE PROTEIN PRECURSOR (CONTAINS: FETAL ANTIGEN 1) IFA1) (DI K) + ADRENAL SPECIFIC 30kd PROTEIN GB: X17544	U15979; [Z12172]	C3l	1090-1403
manic fringe	U94352	C3m	979-1235

TABLE 3 (CONT)

194354 C3n 194354 C3n 194354 C3n 194354 C3n 194354 C3n 194355 C4a 194355 C4d 1943518 C4d 194401 C4k 194401 C4k	Cell Cycle/Growth Regulators	GenBank #	Array Coordinate	Position
Manuace Manu		U94354	C3n	563-857
1,20861 C4a 1,20861 C4b C4b C4c C4	-Wot pathway			
120861 120861 120861 120861 120861 120861 120861 120861 120861 120861 120861 120862 1	WNT9 OR IRP	X07876	C4a	899-1252
X91940 C4C X97657 C44 X97657 C44 X17621 C44 X17622 C41 X17622 C41 X17623 C41 X17623 C41 X17624 C41 X17624 C41 X17625 C41 X17625 C41 X17625 C41 X17626 C41 X17626 C41 X17626 C41 X17626 C41 X17627 C41 X17628 C41 X176	Wotks	L20861	C4b	1036-1281
X97057 C4d Z71821 C4e Z71821 C4e Z71821 C4e Z71821 C4f Z71821 C56 Z71821 C56 Z71821 C56 Z71821 C57 Z71821 C718 Z71821	WNT.RB	X91940	C4c	164-447
271621 C46 137882 C4f 137882 C4f 137882 C4f 148282 C4f 148382 C4f 148382 C4f 148383 C4f 148383 C4f 148384 C5b 148384 C5f 1483	WNT.10R	X97057	C4d	330-635
137882 C41 127882 C41 124163; [U91903; U68057] C42 124163; [U91903; U68057] C44 1241641 C55 1241641 C55 1241641 C56 12416441 C	Wat-13	271621	C4e	569-847
U24163; [U91903; U68057] C49 S4 C44 C4	frizzled	L37882	C4f	1491-1756
C49 C40 C41	related FrzB	U24163; [U91903; U68057]		
U43318 C4h U49262; [U75651] C4j U49262; [U7661] C4j U49262; [U7663] C4j U49262; [U7663] C4j U49262; [U7663] C5j U49262; [U7668] C5j U49262; [U7668] C5j U49262; [U7668] C5j U49262; [U7688] C5j U7707 C29064] C5j U7707 C29067			C4g	590-819
U82169 C4i C4i U49262; [U75651] C4j U46461 C4k U46461 C4k U46461 C4k U46461 C4k U46461 C4k U46461 C4k U43148 C4m U43148 C4m U43148 C4m U43148 C4m U44101 C4m U44101 C4m U44101 C5c U46729 C5c U4672	frizzled 5	U43318	C4h	936-1091
C4 C4 149262; [U75651] C4 14 C4 14 C4 15 C4 16 C4 17 C4 18 C4 19 C5 10 C5 11 C5 11 C5 11 C5 12 C5 13 C5 14 C5 15 C5 16 C5 17 C5 18 C5 18 C5 19 C5 10 C5 10 C5 10 C5 10 C5 11 C5 11 C5 12 C5 13 C5 14 C5 15 C5 16 C5 17 C5 18 C5 18 C5 19 C5 10 C5 11 C5 11 C5 12 C5 13 C5 14 C5 15 C5 16 C5 17 C5 18	omolog (FZ	U82169	C4i	865-1182
138518	dishevelled (DVL) + dishevelled 3 (DVL3)	U49262; [U75651]	C4j	1311-1610
138518 C4 143148 C4m 143148 C4m 143148 C4m 143148 C4m 14401 C4n 14401 C4n 14402 C4n 14402 C5a 14402 C5b 14402 C5c 14403 C5c 14404	dishevelled homolog (DVL)	U46461	C4k	1409-1586
138518 C41 U43148 C4m U43148 C4m U43148 C4m U43148 C4n U43148 C4n U43148 C4n U43148 C4n U43148 C4n U4401 C5a U4401 U4n U41012 U41012 U4n U41012 U41012 U4n U41012 U41012 U4n U41012 U41012 U4n U41012 U41012 U4n U41012 U4n	-Hedgehon pathway			
U43148 C4m U84401 C4n U84401 C4n U84401 C4n U84401 C4n U84401 C5a EIN KINASE RECEPTOR UFO) M76125 C5b IT MANNOSE-6-PHOSPHATE RECEPTOR Y00285; [J03528] C5c VTH FACTOR RECEPTOR-RELATED B- X60592 C5d VTH FACTOR RECEPTOR PRECURSOR (EC U48722] C5f IT ACTOR RECEPTOR PRECURSOR (EC U48722] C5f IN	sonic hedgehod (SHH)	L38518	C4I	164-474
U84401 C4n	patched homolog (PTC)	U43148	C4m	3179-4050
SE SE CSA ETAL ANTIGEN Z29083 C5a ETAL ANTIGEN M76125 C5b SINE-PROTEIN KINASE RECEPTOR UFO) M76125 C5b GEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR Y00285; [J03528] C5c Growth factor receptor II, IGFR-2] X60592 C5c RVE GROWTH FACTOR RECEPTOR-RELATED B- X60592 C5d GROWTH FACTOR RECEPTOR PRECURSOR (EC W3193; [X00588; X00663; C5d C5d GROWTH FACTOR RECEPTOR PRECURSOR (EC U04722] C5d GROWTH FACTOR RECEPTOR PRECURSOR (EC U04707; [Z29064] C5f GEFR) (ERBB1) U07707; [Z29064] C5f 14P PROTEIN) M60459 C5f ROTEIN RECEPTOR M60459 C5f ROTEIN RECEPTOR M60459 C5f ROTEIN RECEPTOR M70707; [Z29064] C5f ROTEIN RECEPTOR M60459 C5f ROTEIN RECEPTOR M7045; [S83182] C5n ATOR M707; [M95667] C5n ATOR M707; [M95667] C5n <t< td=""><td>smoothened</td><td>U84401</td><td>C4n</td><td>503-789</td></t<>	smoothened	U84401	C4n	503-789
M76125 C5a	BECEPTORS			
M76125 C5b IR Y00285; [J03528] C5c X60592 C5d C K03193; [X00588; X00663; C5d C5e U07707; [Z29064] C5e U07707; [Z29064] C5f U12535 C5f L0788 C5f M60459 C5i X65923 C5i X65923 C5i X65923 C5i M1730; [M95667] C5i M1730; [M95667] C5i D14012 C5n D25216 C6b M35410 C6c	STA ONCOFETAL ANTIGEN	Z29083	C5a	748-981
Y00285, [J03528] C5c X60592 C5d C K03193; [X00588; X00663; C5e U07707; [Z29064] C5f U12535 C5f U12535 C5f L07868 C5h M60459 C5i X65923 C5i X65923 C5i X65923 C5i X65923 C5i D14012 C5h D14012 C5h D14012 C5h D14012 C5h D14012 C5h D14012 C5h M35410 C6c C	AXI (TYROSINE-PROTEIN KINASE RECEPTOR UFO)	M76125	CSb	2045-2348
X60592 C5d C K03193; [X00588; X00663; U48722] C5e U47707; [Z29064] C5f U12535 C5f L07868 C5f L07868 C5f M60459 C5f X65923 C5i X65923 C5i X65923 C5i M1773; [M95667] C5i M29366; [M34309] C5m D14012 C5n D49742; [S83182] C6a M35410 C6c	CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR	Y00285; [J03528]	, U	1307-1831
C5d (C5d (C5d (C3193; [X00588; X00663; C5e (U48722] (U48722] (U7707; [Z29064] (U535 (U7535 (U7535 (U75868 (U7688 (U7707; [Z29064] (U7907) (U	[insuline-like growth factor receptor II, IGFR-2]		200	1004-1001
RMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC K03193; [X00588; X00663; C5e 12). (EGFR) (ERBB1) U48722] C5e 12). (EGFR) (ERBB1) U07707; [Z29064] C5f 5 (AF-1P PROTEIN) U12535 C5f 4 L07868 C5f 4 L07868 C5f 4 M60459 C5f 4 K65923 C5f 4 K65923 C5f 4 K65923 C5f 6 C5K C5K 6 M17730; [M95667] C5f CERB-R3) C5m C5m CTIVATOR D14012 C5n COMPLEX ACID LABILE CHAIN D25216 C6b ACTIVATOR M35410 C6c	CDW40; NERVE GROWTH FACTOR RECEPTOR-RELATED B- II YMPHOCYTE ACTIVATION MOLECULE	X60592	C5d	198-605
(AF-1P PROTEIN) (CST 5 (AF-1P PROTEIN) U12535 CST 4 U12535 CST 4 HOPROTEIN RECEPTOR M60459 CSI 4ROPROTEIN RECEPTOR X65923 CSI (ERB-B2) M11730; [M95667] CSI (ERB-B3) M29366; [M34309] C5m (CTIVATOR D14012 C5n ACTIVATOR D49742; [S83182] C6a ACTIVATOR D25216 C6b ACTIVATOR M35410 C6c	EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC	K03193; [X00588; X00663;	CSe	3410-3757
U12535 C5g	-10	U07707; [Z29064]	CSf	1828-2140
4 L07868 C5h HROPROTEIN RECEPTOR M60459 C5i K65923 C5j C5j Z24680 C5k C5j (ERB-B2) M1730; [M95667] C5k (ERB-B3) M29366; [M34309] C5m (CTIVATOR D14012 C5n ACTIVATOR D49742; [S83182] C6a ACTIVATOR LIKE D25216 C6b ACMPLEX ACID LABILE CHAIN M35410 C6c ACOMPLEX ACID LABILE CHAIN M35410 C6c		U12535	C5g	2293-2645
IROPROTEIN RECEPTOR M60459 C5i X65923 C5j Z24680 C5k (ERB-B2) M11730; [M95667] C5l (ERB-B3) M29366; [M34309] C5m CTIVATOR D14012 C5n CTIVATOR LIKE D49742; [S83182] C6a COMPLEX ACID LABILE CHAIN D25216 C6b A35410 C6c C6c	EBB4	L07868	CSh	3570-39 65
K65923 C5j [ERB-B2) C5K (ERB-B3) M1730; [M95667] C5I CTIVATOR D14012 C5n CTIVATOR LIKE D49742; [S83182] C6a COMPLEX ACID LABILE CHAIN D25216 C6b A35410 C6c C6c	ROPROTEIL	M60459	C5i	1423-1740
[ERB-B2) C5K (ERB-B3) M1730; [M95667] C5I CTIVATOR D14012 C5n CTIVATOR LIKE D49742; [S83182] C6a COMPLEX ACID LABILE CHAIN D25216 C6b A35410 C6c C6c		X65923	CSj	8-344
(ERB-B2) M11730; [M95667] C5I (ERB-B3) M29366; [M34309] C5m CTIVATOR D14012 C5n CTIVATOR LIKE D49742; [S83182] C6a COMPLEX ACID LABILE CHAIN D25216 C6b A35410 C6c	GARP	Z24680	C5k	3399-3777
RB-B3) M29366; [M34309] C5m TIVATOR D14012 C5n TIVATOR LIKE D49742; [S83182] C6a OMPLEX ACID LABILE CHAIN D25216 C6b M35410 C6c	HFR2 (ERB-B2)	M11730; [M95667]	CSI	2556-2722
TIVATÓR D14012 C5n TIVATOR LIKE D49742; [S83182] C6a OMPLEX ACID LABILE CHAIN D25216 C6b M35410 C6c	HER3 (ERB-B3)	M29366; [M34309]	C5m	3886-4139
TIVATOR LIKE D49742; [S83182] C6a OMPLEX ACID LABILE CHAIN D25216 C6b M35410 C6c	HGF ACTIVATOR	D14012	C5n	1487-1845
OMPLEX ACID LABILE CHAIN D25216 C6b M35410 C6c		D49742; [S83182]	C6a	311-595
M35410 C6c	-	D25216	Ceb	1509-2669
		M35410	Cec	680-1071

TABLE 3 (CONT)

Cell Cycle/Growth Requiators	GenBank #	Array Coordinate Position	Position
HORMONE-DEPENDENT INSULIN-LIKE GROWTH	M31159; [M35878]	Ced	451-744
INFRIDATION OF THE PROPERTY.	M62403	C6e	657-967
CERPS	M65062	Cef	356-602
IGEBP6	M62402	Ceg	345-536
4-LIKE GROWTH FACTOR I RECEPTOR	X04434	Ceh	3413-3904
BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR	M37722; [X66945;		
(BFGF-R) (EC 2.7.1.112) (FMS-LIKE TYROSINE KINASE-2) (C-FGR)	M63887; M63888;		
:BR) (FLT2). (HBGF-R-ALPHA-A1) (HBGF-H-ALPHA- A A 2) : FOEB SECPETED FORM (M34188)	M63889;M34186; M34641J	•	
AZ) (HBGF-R-ALPRA-AS) + FGFR SECNE ED FOLIM (MO4109)		Cei	1746-1967
NERVE GROWTH FACTOR RECEPTOR	M14764	Cej	2762-3242
PNGFR-AI PHA	M21574	C6K	5118-5583
DOCE BETA	M21616	Cel	842-1133
transmembrane receptor precursor (PTK7); COLON CARCINOMA	U33635; [U40271]		
KINASE-4 (CCK4)		C6m	3507-3784
SEX GENE	X87852	Cen	209-433
TRANSFORMING GROWTH FACTOR-BETA TYPE III RECEPTOR	L07594	C7a	3358-3592
TRANSMEMBRANE PROTEIN TMP21	X97442	C7b	380-1176
HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR	X03541		
(EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN)			
(P140-TRKA) + trk-T3 (P68 TRK-T3 ONCOPROTEIN)			0460
		0/10	1010-2110
trk-T3 (P68 TRK-T3 ONCOPROTEIN)	X85960	C/a	2111-262
trk-8	U12140	C7e	1006-1384
1rk-C	U05012	C7f	359-765
TIMOR NECROSIS FACTOR RECEPTOR 1	M33294	C7g	1570-1817
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR	M32315; [M55994]		
NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2)			3350.35/3
(P/5) (CD120B) (INFRZ) (INFBA).	#179770: fVA6E99:	5	2000
HE LINOIC ACID HECEP LON ALPHA I (NAN-ALPHA I) + FWIL-NAN nrotein	[X06614]	C7i	2935-3238
retinoic acid receptor alpha [RETINOIC ACID RECEPTOR RXR-ALPHA	X52773	67	250 646
(RXRA)]		5	222-010
retinoic acid receptor epsilon [RETINOIC ACID RECEPTOR BETA-2 (RAR X07282; [Y00291] BETA-2) (RAR-EPSILON)]	X07282; [Y00291]	C7k	1315-1633
retinoic acid receptor gamma [RETINOIC ACID RECEPTOR GAMMA]	M24857; [M38258;	i	
	M57/07; M320/4]	1/0	1569-1834
retinoic acid receptor rxr-beta [RETINOIC ACID RECEPTOR HXH-BETA]	M84820; [X63522]	E/O	643-1135

TABLE 3 (CONT)

Call Cycle/Growth Requiators	GenBank #	Array Coordinate	Position
		_	5117-5435
THROMBOPOELLIN RECEPTION			
QUADRANT D			
CELL ADHESION MOTILITY, AND INVASION			
CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN (CSPCP)	M55172		
(AGGRECAN 1)(CHONDROITIN SULFATE PROTEUGLYCAN CORE		D1a	6705-6956
PROJEIN 1)	J04599	D1b	854-1129
byglycan		D1c	596-960
CU34		D1d	105-1163
DROITIN/DER	M14219	910	712-896
PROTEIN (DECORIN) (PG-S2) (PG40)	D21337	D1f	5342-5588
COLLAGEN (~6000BP)	-	D1g	428-741
collagen type I		D1h	3604-3751
Collagen type II arp alpha 1		D1i	3867-4046
Collagen type III pro-aprila-1		D1j	882-1113
Collagen type IV alpha 3		D1k	2296-2545
Collagen type IV alpha 1		D11	316-688
Collagen type vi alpha i		D1m	203-396
Collagen lype VI appliand		D1n	640-1487
Collagell type VI alpha-1	X57527	D2a	612-1772
Collagen type vill alpha 1		D2b	2864-3091
Collagen type At alpha-1		D2c	4473-4769
Collagen type At pro-apria-2		D2d	4816-5991
collage I type Avi alpha		D2e	2300-2539
LAMAAH (JAMAA)	[X91171]	D2f	1018-1388
I AMBO (I AMININ)		D2g	3871-4158
laminia R1	M61916	D2h	3177-3554
laminia Ro	J03202	D2i	2878-3232
Inmining 37KD RECEPTOR	U43901	D2j	460-812
ומוווווון, אותם וובטבו וכוי	U86759	D2k	859-1147
neithr-z	M30269	D2I	2120-2428
minogen Trainscin O	X78565	D2m	6652-6924
TENASCIN-D	X98085	D2n	3916-4165
VERSICAN [isoforms, V1, V2, V3]	U16306; [X15998; U26555;	Š	180.074
	D3Z039	USa	10-00

TABLE 3 (CONT)

	: .		Decition
Cell Cycle/Growth Regulators	GenBank #	Array Coordinate Position	TOSTECT
ROTEIN ACIDIC AND RICH IN	J03040		
CYSTEINE) (OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN		D3b	280-642
BM-40).	X14787	D3c	3187-3450
	L12350	D3d	3151-3531
EADING FACTOR) (S-	X03168	J36	3721-4093
PROTEIN) (CONTAINS: SOMALOMEDIN B)	Y02761	D3f	6163-7290
	1112431-[[129943]	D3a	1006-1384
RNA-binding protein Hel-NZ; ELAV-IIRe Heulolia protein i	M85289	Dah	1232-1389
ULFATE PROTECUELIONIN (1101 OF)	X68742	D3i	2690-2976
integrin alpha [very late antigen-2 (vla-2)/collagen receptor alpha-2	M28249; [X17033]	D3i	2367-2664
subunit	M59911	D3K	2564-2944
integrin alpha3	1 12002: [X16983]	D3I	2709-3063
- 1	X06256	D3m	2094-2367
Integrin alpha Introduction archive account	X53586: [X59512]	D3n	3642-3988
Integrin alphab	X74295	D4a	255-591
Integrin alpha / D	L36531	D4b	2709-3063
integrin alphao	D25303; [L24158]	D4c	706-980
integrin alphas	L25851	D4d	2279-2529
inegnii alpitat	M34189	D4e	701-1301
	J02703; [M25108]	D4f	2038-2373
5	X53587: [X52186]	D4g	5357-5697
integrin beta4	J05633	D4h	2279-2528
integrin belab	M35198	D4i	1619-1901
integrili berao	M62880	D4j	2562-2944
integrin beta	M73780	D4k	22-877
Integrili Detad	L13616	D4I	2179-2631
Integrin-linked kinase (ILK)	U40282	D4m	1245-1530
Protein tyrosine kinase Pyk2 (Cell adhesion kinase-beta, CAK-beta) (FAK2) U43522; [L49207]	U43522; [L49207]		0000
		D4n	2020-0000
Davillin	U14588	D5a	1260-1644
Zwin Zwin.9	X94991; [X95735]	DSb	585-1514
Zwin related protein ZRP-1	AF000974	D5c	1240-1466
Lyxii Telated Protein 21 ii i	U37139	DSd	606-1504
Deta 3-chochoch.	U59752	D5e	43-338
Cyloricality, door prince process	M38690	DSf	372-962
Exio (cytoxillin 2)	X51521	D5g	1611-1883

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	GenBank #	Array Coordinate	Position
MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like	Z22664; X72657;		
protein)(neurofibromatosis 2)	L27133	D5h	355-674
L1CAM	M74387	D5i	3197-3485
N-CAM INEURAL CELL ADHESION MOLECULE,	X16841	i	
PHOSPHATIDYLINOSITOL-LINKED ISOFOHM; CD56]		USJ	2338-2646
NINJURIN-1	U72661	D5k	212-492
opioid binding cell adhesion molecule	L34774	D5I	115-728
DCC	X76132	D5m	893-1189
P37NB	U32907	D5n	95-456
PLEXIN	U52111	D6a	585-1514
semaphorin (CD100)		D6b	2517-2921
semaphorin E	AB000220	D6c	2949-3181
semaphorin III	L26081	peq	899-1152
semaphorin V	U33920	D6e	177-442
SEMAPHORIN-1	U38276	Def	488-653
TAX1, AXONIN-1/TAQ1	X85978	D6g	209-433
LAR	Y00815	Deh	5799-6049
HYALURONAN RECEPTOR (RHAMM)	U29343	D6i	2496-2798
PLATELET GLYCOPROTEIN IV (GPIV) (GPIIIB) (CD36 ANTIGEN) (PAS	M24795		
IV) (PAS-4 PROTEIN)		D6j	554-806
caveolin-2	AF035752 U32114	D6k	1340-1519
caveolin-1	Z18951 S49856	Del	62-413
ANGIOGENESIS REGULATORS			
VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2	L04947; [X61656]		
PRECURSOR (EC 2.7.1.112) (VEGFR-2) (KDR) (KINASE INSERT			0200 0000
NASCIII AB ENDOTHEI IAI GROWTH FACTOR RECEPTOR 3	X68203- [X69878- [143143]		0000-0007
PRECURSOR (EC 2.7.1.112) (VEGFR-3) (TYROSINE-PROTEIN KINASE			
RECEPTOR FLT4, CLASS III).		D6n	4236-4402
FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE- PROTFIN KINASE RECEPTOR FLT3) (STEM CELL TYROSINE KINASE	U02687		
1) (STK-1) (CD135 ANTIGEN).		D7a	2491-2965
TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC	X60957 [S89716]		
2.7.1.112).		D7b	3114-3536
TYROSINE-PROTEIN KINASE RECEPTOR TIE-2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TEK) (P140 TEK)	L06139		
(TUNICA INTERNA ENDOTHELIAL CELL KINASE).		D7c	3243-3586

TABLE 3 (CONT)

Cell Cycle/Growth Regulators	Genbank #	Array Coordinate Position	Position
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-1U48801; [U43368] B) + VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR	U48801; [U43368]		
		D7d	158-648
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF- 043142	U43142		
PROTEIN (VRP) (FLT4 LIGAND).		D7e	1165-1559
PLACENTA GROWTH FACTORS 1 AND 2 PRECURSOR (PLGF-1/	X54936		
			1098-1371
KINE PRECURSOR (FLT3/FLK2 LIGAND).	U04806; [U03858]	D7g	29-362
	U83508		1749-2031
ACTOR RECEPTOR [Golgi	U28811; [U64791]	D7i	3279-4140
FGFB3 (FLG-2)	M58051; [X58255]	D7j	323-896
	L03840	D7k	1503-1743
3LAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (FGFR-	U11814; [M80634; X52832; M35718: M87771; M87772]		
(FGFR2) (BEK) (BFR-1) (KSAM-1) + K-SAM; K-SAM-III; K-SAM-IV	•	D7I	753-1189
VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECIPESOR (EC 2.7.1.12) (VEGFR-1) (TYROSINE-PROTEIN KINASE	U01134; [X51602]		
RECEPTOR FLT) (FLT-1) (SFLT)		D7m	1288-1604
HOMEOBOX PROTEIN HOX-D3 [HOX 4A]	D11117	D7n	4200-4447
QUADRANT E			
INVASION REGULATORS			
	X05231	E1a	512-836
	J03210, [J05471]	Etb	477-778
	X05232	E1c	331-1491
MMP-7 (matrilysin)	X07819	E1d	335-738
MMP-8 (collagenase-2)	J05556	E1e	532-865
MMP-9 (gelatinase B)	J05070, [D10051]	EI	1012-1346
MMP-10 (stromelysin-2)	X07820, [M30461]	E1g	387-1319
MMP-11 (stromelysin-3)	X57766	E1h	263-1508
MMP-12 (metalloelastase)	L23808	ΕŢ	275-787
MMP-13 (collagenase-3)		E1j	463-761
MMP-14 (MT1-MMP)	D26512, [X83535]	E1¢	413-749
MMP-15 (MT2-MMP)	Z48482	E11	1210-1456
MMP-16 (MT3-MMP)	D50477	E1m	991-1226
MMP-17 (MT4-MMP)	X89576	E1n	630-1830
MMP-19	X92521	E2a	1383-1655

TABLE 3 (CONT)

	Company #	Array Coordinate	Docition
Cell Cycle/Growth Regulators	AIIK #	ay cool dinate	10000
TIMP-1 (enghroid potentiating activity, EPA)		EZD	784-481
	J05593	E2c	403-694
non-induciple dene 5 min-5)	Z30183	E2d	346-587
TIME S (IIII Ogen Fill account going of the S (IIII) S (IIII)		E2e	445-671
I IMIT-4	L20471	E2f	23-354
UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC	M15476		
3 4 21 73) (UPA) (U-PLASMINOGEN ACTIVATOR)		E2g	824-1120
TISSUE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC	M15518; [X07393; M181821	E2h	1221-1577
AIOU).	X05199	E2i	1859-2162
VATOR INHIBITOR-1 PRECURSOR,	X04429	E2i	1195-1342
PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2)	M18082;[J02685]	E2k	378-954
PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI)	M68516; [J02639]		
(PROTEIN C INHIBITOR) (PLASMINOGEN ACTIVATOR INHIBITOH-3)		E2I	8035-8423
UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI- ANCHORED FORM PRECURSOR (U-PAR) (MONOCYTE ACTIVATION	U08839 [M83246; X51675]		0
ANTIGEN MO3) (CD87 ANTIGEN)		E2m	/49-1043
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 DEPCY. IBSOR (I RB) (AI PHA-2-MACROGLOBULIN RECEPTOR) (A2MR)	X13916		
		E2n	5439-5742
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2	U04441	E3a	1365-2162
AI BLA 2 MACROGI OR II IN PRECIPSOR (ALPHA-2-M)	M11313	E3b	3972-4325
PLATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS:	M54995; M38441		
AFFINITY PLATELET FACTOR IV (LA-PF4), BETA-			
THROMBOGLOBULIN (BETA-TG), NEUTHOPHIL-ACTIVATING PEDTING SAMAP-20)		E3c	63-252
ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN	M63959	י ט	740-800
RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (HAP)	V47690	Loa	200
NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.5) (NUK A) (NUPKINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN)	079/1	13°	245-612
(METASTASIS INHIBITION FACTOR NM23) (NM23-H1).			210 012

TABLE 3 (CONT)

		A man Condingto	Docition
Cell Cycle/Growth Regulators	Genbank #	Array Cool ulliate r Osliton	I Control
NUCLEOSIDE DIPHOSPHATE KINASE B (EC 2.7.4.6) (NDK B) (NDP	L16785; [M36981]		
KINASE B) (NM23-H2) (C-MYC PURINE-BINDING TRANSCRIPTION		E3f	69-351
nm23-H4; NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6)	Y07604	E3q	141-448
(NUCLEOSIDE 5-DIPHOSPHALE PHOSPHOSPHOLINAS)	U43527	E3h	116-454
malignant melanoma metastasis-suppressor (1900-1) gons		E3i	957-1825
MEI ASI ASIS-ASSOCIALED MITAL		E3j	1068-1200
PROSIATE-SPECIFIC MEMbrane Anticon (1907)		E3k	640-958
metallopiotease/dislinegimy/systems			
י אוור ו	X06820	E3i	53-1648
(The Carlotte Carlotte (NaC)	L25081	E3m	637-1473
(H9); SMALL G		E3n	900-1228
mod		E4a	33-388
Rho6 protein		E4b	75-377
Rho7 protein		E4c	209-534
Hhos protein	M29870; [M31467]		
HAN-HELATED OF BOTOLINGIA TOXING COLOURS OF THE COL		E4d	55-429
(RAS-LINE PHOTEIN 1023)	M64595; [M29871]	E4e	31-1185
HAV-HELATED OS BOTOCINOM TOXIN COLOR		E4f	80-350
ras-like protein 1010	235227	E4g	491-759
Small GIra		E4h	130-361
morrell collections protein kinase of 60BOCK	U43195	E4i	3793-4233
Pho-associated, colled-coll collianing process which are processed and a process which are processed as a process which are processed as a pr	U02570	E4j	864-1182
CDC42 to Frase-activating protein	U82532	E4k	309-554
GDI-dissociation Infilibitor Fillodoliganimia	U16296	E4I	4275-4645
PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE	U11690	<u> </u>	3033 4165
FACTOR(RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN)	X78817	E4n	781-1170
HHO-GAP HEMATOPOIETIC FNOTEIN OF (1.13) (W. C.C.).	1.20688	E5a	322-600
rho GDP-dissociation intributed by the CLY-devy	X69550	ESb	328-624
SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1) (P65-	U24152	ζ 11	756-1055
PAKI (P21- ACTIVATED KINASE) (ALPHA-PAK)		1	2001 000
p21-activated protein kinase (Pak2)	U24153	E5d	335-671
CELL CELL INTERACTION			
CADHERIN-2 (N-CADHERIN)	M34064 [X57548; X54315;	1	0,00
	S42303]	E5e	942-1299
CANHERINA PLACENTAL -CADHERIN PRECURSOR (P-CADHERIN)	X63629	Esf	542-835

TABLE 3 (CONT)

	# -1 C	Array Coordinate	Position
	Genbank #	Allay Cooluliate	1031101
HERIN-4 RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-	L34059	E5g	1172-1425
CADHERIN-5 VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-X79981; [X59796]	X79981; [X59796]	Esh	1607-1769
104 70	D31784	E5i	2119-2443
	L34060	E5j	1069-1347
COBI AST.CADHEBIN) (OB-CADHERIN)	L34056	E5k	1778-2076
IN-12 (BR-C	L34057; [L33477]	E51	657-903
RSOR (TRUNCATED-CADHERIN)	L34058; [U59289; U59288]	E5m	949-1187
	D83542	Esn	228-456
(CADHERIN-14) (CADHERIN-15) ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN) (ALPHA E-	D13866 [D14705 L23805;	E6a	55-492
CATENIN)	M94151	E6b	2296-2545
ALPHA-CATENIN RELATED PROTEIN (CATENIN ALL LINE)	X87838 [719054]	E6c	2061-2463
BETA-CATENIN	M23410	E6d	2000-2312
PLAKOGLOBIN (DESMOPLANIN III)	M74088: [M73548]	E6e	7992-8326
APC (DP2.5) neuroendocrine-dlg (NE-dlg) a novel human homolog of the Drosophila	U49089		
discs large (dlg) tumor suppressor protein interacting with the Al C protein		E6f	2210-3116
ADV of obeside to ADV	U24166	E6g	488-796
=	L11370	E6h	1246-1605
protocadherin 42	L11373	Eei	1018-1388
protocadherin 43	M77830	E6j	6987-7826
desmoplakin i	U53786	E6k	5583-5788
envoplakin (EVFL)	M63618	E6l	5680-6055
Julious peripingola crimgon	Z26317 [S64273]	E6m	2819-3135
desillogicii E	X56654	E6n	25/8-2889
desmoglein type 1	X72925	E7a	475-1154
desmocollin type 1	X83929; [D17427]	E7b	608-1607
desmocollin type 3 + desirocollins type 4	X56807	E7c	802-1115
EPHRIN-A1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE	M57730 M37476		
KINASE LIGAND 1) (LERK-1) (IMMEDIATE EARLT RESPONSE PROTEIN R61) (TUMOR NECROSIS FACTOR, ALPHA-INDUCED			
PROTEIN 4)		E/d	124-1002
	U26403	Е7е	375-1325
KINASE LIGAND // (LENY-/) (AL-1).			

TABLE 3 (CONT)

136395 136395 [M27281] [U50330]				
L38734 E L38734 E U66406 L66406 K59371 M36395 L41939 L41939 L41939 L41939 L41939 L41939 L41939 M77349	h Regulators	GenBank #	Array Coordinate	Position
L38734 E U66406 U66406 L46636 L40636 L40636 U07695 M16591 M30704 M15530 M15530 M15530 M77349 pCP- M22488; [U50330] M22489 M22489 M22481 D49493 D30751; [M22490]	SOR (EPH-RELATED RECEPTOR TYROSINE	U09304	E7f	507-1186
AL CELL M59371 M36395 AL CELL X95425 MOLOGY 7). L40636 L41939 U07695 U07695 U07695 U07695 M30704 M15530 M15530 M15530 M15530 M15530 M15530 M22589 DR (VEGF) M32977; [M27281] M22489 M22489 M22489 M22489 M22489 D30751; [M22490]		L38734	F7n	442-560
AND P60- M16591 AND P60- M22489; [U50330] M22489 M22491 M22491 M22491 M22491 M22490]	1	007001	D	
AL CELL M59371 M36395 AL CELL X95425 MOLOGY 7). L40636 141939 U07695 U07695 U07695 M30704 M15530 M15530 M15530 M15530 M15530 M15530 M15530 M22489; [U50330] M22489; [U50330] M22489	OR TYROSINE	U66406		
AL CELL X95425 MOLOGY 7). L40636 U07695 AND P60- M16591 AND F60- M16591 M827349 M822489 M22489	KINASE LIGAND 8) (LEMN-8) (ET N-NELATED NECET 10).		E7h	2056-2282
AL CELL X95425 MOLOGY 7). L40636 L41939 U07695 U07695 M30704 M30704 M15530 M15539 M61176 X52599 X52599 M77349 M22489; [U50330] M22489 M22491 M22491 M22491 M22491 M22491 M22490]		M59371 M36395		
NEMASE RECEPTOR EHK-1) (EPH HOMOLOGY OR PROTEIN- TYROSINE KINASE HEK7). L40636 L41939 L41939	(TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL		Ë	340 1426
TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) NE-PROTEIN KIMASE RECEPTOR EHK-1) (EPH HOMOLOGY NE-PROTEIN KIMASE RECEPTOR EHK-1) (EPH HOMOLOGY TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) NE-PROTEIN KIMASE RECEPTOR (EC 2.7.1.112) TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) NE-PROTEIN KIMASE RECEPTOR HITK) NE-PROTEIN KINASE RECEPTOR HITK) NE-PROTEIN KINASE RECEPTOR HITK) NE-PROTEIN KINASE RECEPTOR HITK) NE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-M16591 EMOPOIETIC CELL KINASE). RANT F H FACTORS/CYTOKINES H FACTORS/CYTOKINES REGULIN RANT F H FACTORS/CYTOKINES REGULIN RASSOR REGULIN RASSOR REGEPTOR PRECURSOR (VEGF) M30704 M15530 M77349 M77349 MA2489 MORPHOGENETIC PROTEIN 2A MA2489 MORPHOGENETIC PROTEIN 3B MORPHOGENETIC PROTEIN 4 (BMP-2B) MORPHOGENETIC PROTEIN 3B MORPHOGENETIC PROTEIN 3B MORPHOGENETIC PROTEIN 3B MORPHOGENETIC PROTEIN 3B MORPHOGENETIC PROTEIN 4 (BMP-2B) MORPHOGENETIC PROTEIN 4 (BMP-2B) MORPHOGENETIC PROTEIN 4 (BMP-2B) MORPHOGENETIC PROTEIN 4 (BMP-2B) MA2489	KINASE).		E/1	0741-647
IN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY OR PROTEIN- TYROSINE KINASE HEK7). CEPTOR 1 PRECURSOR (EC 2.7.1.112) IN KINASE RECEPTOR EPH-2) (NET). CEPTOR 2 PRECURSOR (EC 2.7.1.112) IN KINASE RECEPTOR HTK). IN KINASE RECEPTOR HTK). IN KINASE RECEPTOR HTK). IN KINASE HECEPTOR HIKE). IN KINASE HECEPTOR HIKE HIKE HIKE HIKE HIKE HIKE HIKE HIKE	TYPE-A RE	X95425		
(AND P60- M16591 (AND P60- M16591 (M30704 M15530 (M15530 M61176 (M52599 (M7349 (M7349 (M2248) (M2248) (M22491 (M22491 (M22491)			E7j	644-1300
AND P60- M16591 M30704 M15530 M15530 M15530 M61176 X52599 N77349 M77349 M2248; [U50330] M22489 M22491 M22491 D30751; [M22490]	EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112)	L40636	רשני	008-1460
AND P60- M16591 M30704 M15530 M61176 M61176 X52599 N77349 M77349 M22489; [U50330] M22489 M22491 M22491 M22491 M22491 M22491 M22491	(TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (NE I).		L/ h	200
AND P60- M16591 M30704 M15530 M61176 X52599 DR (VEGF) M32977; [M27281] M77349 M22488; [U50330] M22489 M22491 M22491 D30751; [M22490]	EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112)	L41939	E71	454-1225
AND P60- M16591 M30704 M15530 M61176 X52599 X52599 X75259 M77349 M77349 M77349 M2248; [U50330] M22481 M22491 M22491 M22491 M22491 M22491	EPHBIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112)	U07695		
SINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60- M16591	TYBOSINE-PROTEIN KINASE RECEPTOR HTK).		E7m	/56-1652
DRANT F THE FACTORS/CYTOKINES THE FACTORS/CYTOKINES M30704 I (B-cell growth factor) M15530 I (B-cell growth factor) M61176 NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] ULAR PERMEABILITY FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP- M22488; [U50330] M22489 MORPHOGENETIC PROTEIN 2A M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]	TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-	M16591	E7n	194-1187
Name				
DRANT F TH FACTORS/CYTOKINES M30704 IREGULIN M15530 I (B-cell growth factor) M61176 NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] ULAR PERMEABILITY FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP- M22488; [U50330] MORPHOGENETIC PROTEIN 2A M22489 MORPHOGENETIC PROTEIN 3 M22491 MORPHOGENETIC PROTEIN 3 D39751; [M22490] MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]				
TH FACTORS/CYTOKINES M30704 IREGULIN M15530 I (B-cell growth factor) M61176 NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] ULAR PERMEABILITY FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 2A M22488; [U50330] MORPHOGENETIC PROTEIN 3 M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]	OUADRANT F			
REGULIN M30704 (B-cell growth factor) M6176 (B-cell growth factor) M6176 (B-cell growth factor) M6176 NGF X62599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] ULAR PERMEABILITY FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 2 M22481 MORPHOGENETIC PROTEIN 3 M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490] MORPHOGENETIC PROTEIN 5 D30751; [M22490] MORPHOGENETIC PROTEIN 5 D30751; [M22490] MORPHOGENETIC PROTEIN 6 M20751; [M22490] MORPHOGENETIC PROTEIN 7 M20751; [M22490] MORPHOGENETIC PROTEIN 7 M20751; [M22490] MORPHOGENETIC PROTEIN 8 M20751; [M22490] MORPHOGENETIC PROTEIN 9 M20751; [M22490] MORPHOGENETIC PROTEIN 9 M20751; [M20751] MANDELIC PROTEIN 9 M20751; [M20751] M20751 M20751 M20751 M20751	GROWTH FACTORS/CYTOKINES			
1 (B-cell growth factor) M15530 NGF M61176 NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-M22488; [U50330] M77349 MORPHOGENETIC PROTEIN 2AMORPHOGENETIC PROTEIN 3 M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]	AMPHIREGULIN	M30704	F1a	511-837
NGF M61176 NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] **ULAR PERMEABILITY FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-M22488; [U50330] M22489 MORPHOGENETIC PROTEIN 3 M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]	BCGE1 (B-cell growth factor)	M15530	F1b	13-248
NGF X52599 ULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) M32977; [M27281] ULAR ENDOTHELIAL GROWTH FACTOR) (VPF). M77349 MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP- M22488; [U50330] M22488; [U50330] MORPHOGENETIC PROTEIN 2A M22491 MORPHOGENETIC PROTEIN 3 D49493 MORPHOGENETIC PROTEIN 4 (BMP-2B) D30751; [M22490]		M61176	F1c	982-1265
In PRECURSOR (VEGF) M32977; [M27281] M77349 M22488; [U50330] M22489 M22491 M22491 M22491 D30751; [M22490]	BETA NGF	X52599	F1d	360-1339
M77349 M77349 M22488; [U50330] M22489 M22489 M22491 M22491 D30741; [M22490] M204493 M204493 M204493 M204490]	VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF)	M32977; [M27281]	F1e	198-622
Ilagen C-proteinase) (pCP- M22488; [U50330] M22489 M22491 M24943 D30751; [M22490]	(אאסטטראוון בווייינים איניים איני מוקאים	M77349	F1f	705-1703
A M22489 M22491 B D49493 (BMP-2B) D30751; [M22490]	BONE MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-	M22488; [U50330]	Į.	4000
M22489 M22491 B D49493 (BMP-2B) D30751; [M22490]		007001	71g	702-1030
M22491 B D49493 (BMP-2B) D30751; [M22490]	BONE MORPHOGENETIC PROTEIN 2A	M22489		100 100
BMP-2B) D30751; [M22490]	BONE MORPHOGENETIC PROTEIN 3	M22491	F1i	1458-1/31
D30751; [M22490]	BONE MORPHOGENETIC PROTEIN 3B	D49493	F1	16188-16418
1100011	BONE MORPHOGENETIC PROTEIN 4 (BMP-2B)	D30751; [M22490]	F1k	943-1321
IMDUS 14	BONE MORPHOGENETIC PROTEIN 5	M60314	F11	1679-1982

TABLE 3 (CONT)

	# 2400	Array Coordinate	Docition
n Regulators	# 41	y cool annace	4007 4007
BONE MORPHOGENETIC PROTEIN 6	M60315	rlm	106/-132/
ETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1)	M60316	F1n	451-691
FTIC PROTEIN 8 (OSTEOGENIC PROTEIN 2)	M97016	F2a	1345-1645
	L42379	F2b	825-1213
SOEDRIM B AND C	A26792	F2c	213-448
OWTH FACTOR	M92934	F2d	1459-1748
	X04571	F2e	4164-4434
ROWTH FACTOR		F2f	1905-2146
	M65199	F2g	338-570
	J05081	F2h	1428-1685
BGF-1)	X51943; [M13361; X65778]		
(ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-		F2i	1131-1502
ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- DETA).			
FGF2; HEPARIN-BINDING GROWTH FACTOR 2 PHECURSON (PROSETATEORIN) (HRGE-2) (BASIC FIBBORI AST GROWTH FACTOR)	MZ/300		
(PROGING IN): (IEC. 2) (SINGE INCESSED IN THE PROGING IN THE PROGI		F2j	1384-1646
FGF-3 INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR	X14445		
(FIBBOBLAST GROWTH FACTOR-3)(HBGF-3).		F2k	189-940
FGE-5- FIBROBLAST GROWTH FACTOR-5 PRECURSOR (HBGF-5).	M37825	F2I	603-1086
FGF-6; FIBROBLAST GROWTH FACTOR-6 PRECURSOR (HBGF-6)	X63454	: C	207 456
		rzin	004-707
(ERATINOCYTE GROWTH FACTOR PRECURSOR (KGF)	M60828	F2n	522-955
FIBRUBLAST GROWTH FACTOR 1/1. ECT. 1	U36223		
(AIGE) (HBGE-8) (FIBROBLAST GROWTH FACTOR-8)		F3a	32-3106
FGF-9: GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST	D14838		
GROWTH FACTOR-9) (HBGF-9).		F3b	110-949
	U66197	F3c	17-566
CONF	L19063	F3d	248-390
GLIA MATURATION FACTOR beta	HG563 [M86492;		
	AB001106]	F3e	203-434
RECOMBINANT GLIAL GROWTH FACTOR + NEU DIFFERENTIATION	L12260; U02326; M94165	} 101	1060-1469
FACTOR + HEREGULIN		10.1	1003-1432
TRANSFORMING GROWTH FACTOR-BETA-2 (glioblastoma-derived t-	M19154; [Y00083]	F30	1538-1878
CELI SUPPLESSOI IACCOI) CEDOMATH INHIBITORY EACTOR (METAL! OTHIONEIN-III) (MT-III)	D13365: [M93311]	F3h	4-1052
GNOWITH INTINGIOUS LANGUAGE (METALESCOTTO)			

TABLE 3 (CONT)

		A	Desition
Cell Cycle/Growth Regulators	GenBank #	Array Coordinate Position	FOSITION
PI FIOTROPHIN PRECURSOR (PTN) (HEPARIN-BINDING GROWTH-	M57399; [X52946; D90226]		
ASSOCIATED MOLECULE) (HB-GAM) (HEPARIN-BINDING GROWTH			
FACTOR 8) (HBGF-8) (OSTEOBLAST SPECIFIC FACTOR 1) (OSF-1)			
(HEPARIN-BINDING NEURITE OUTGROWTH PROMOTING FACTOR 1)		F3i	602-847
(HBMT-1). FARI V GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24)	M62829; [X52541]		
(TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225)		E3i	989-1276
(AT225).	1171470	2	211
HEPATOCYTE GROWTH FACTOR-LIKE (macrophage-stimulating	M/41/8	F3k	1643-2015
protein (MST1))	D16431	F3I	359-625
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR)	M60718		
		F3m	1549-1970
OF ACOMICTANTAGOINST	U46010	F3n	895-1051
COMPETITIVE HEPATOCYTE GROWTH FACTOR ANTAGONIST. AN	M77227		
FACTOR PRECURSOR (SCATTER FACTOR) (SF) (HEPATOPOEITIN A)		Ĺ	9901 200
		r4a	947-1900
IEN GAMMA ANTAGONIST CYTOKINE	A25270	F4b	395-685
	M27544; [M37484]	F4c	652-919
MITTER CLIVIN 4 RECEPTOR ANTAGONIST	M63099	F4d	225-1294
INTERPEDIAL SECENTOR	M20566	F4e	2359-2823
INTERLEGINA OF CETTON	X02851	F4f	1107-1473
INTERLEDINI IL-1 ALTIA	K02770	F4g	917-1208
INTERLEUKIN IL-18ETA	A14844	F4h	181-436
INTERLEDININ IL-2	M14743; [M17115]		
STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-			
CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR)		F4i	390-608
(MCGr) (ILS).	M13982	F4j	216-459
INTERLEUKIN IL-5 (B CELL DIFFERENTIATION FACTOR I) (T-CELL	i	F4k	35-279
REPLACING FACTOR) (EUSINOPHIL DIFFERENTIATION FACTOR	X04602: [M14584]		
INTERLEUKIN-6 PRECORSON (IL-9) (B-CELE STIMOESTED (1707):		F4I	130-555
z) (BSP-2) (INTERT ELICITIES ELICITIES (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	J04156	F4m	174-447
INTEDICION IL 9 (DAD)	X17543; [M30134]	F4n	156-399
-16	M57627	F5a	442-648
INTER FIKIN II -11 [adipogenesis inhibitory factor]	M57765	F5b	132-460
ر ا	M65291	F5c	066-009

TABLE 3 (CONT)

	GanBank #	Array Coordinate	Position
in Regulators		FSd	622-848
(NKST, P4U)		F5e	285-743
		F5f	1181-1562
	114407	F5a	338-695
INTERLEUKIN IL-13	U32659	F5h	257-578
EEBON AI PHA	[100207]	F5i	89-430
FEBON RETA 1		F5j	345-730
EERON GAMMA		F5k	391-586
EERON, INDITICIBLE PEPTIDE	X02492	FSI	372-550
	X13967; [M63420]	F5m	1810-2239
	M25639	F5n	256-476
IBITE PROMOTING FACTOR(NEXIN), dia derived	A03911	F6a	667-915
ROTROPHIC FACTOR)	X53655; [M37763]	F6b	112-416
NT 4 (NT 5) + NT-6	M86528; S41541; [S41540;		
		F6c	721-1079
	U41745	F6d	255-1326
PLOTE SECULE DIVIDENCE OF SECULATION A CHAIN	X06374	F6e	522-955
GROWTH FACTOR, B CHAIN PRECURSOR	X02811; [X02744;		1
DGF-2) (BACAPLERMIN) (C-SIS)	M12783]	F6f	1663-2125
mulating factor homologue)	L36034	F6g	346-1241
SOLITA (pilo di comenza di comenz	U16752; [L36033]	F6h	1053-1481
STEM CELL FACTOR (C-KIT LIGAND)	M59964	F6i	898-1283
T CELL RECEPTOR VARIABLE REGION	M21626	F6j	273-504
TDGF1 (TERATOCARCINOMA-DERIVED GROWTH FACTOR 1)	M96956; [M96955]		
(EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN CR1)			
(CRIPTO-1 GROWTH FACTOR) (CRGF) + TDGF2			
(TERATOCARCINOMA-DERIVED GROWTH FACTOR 2) (EPIDEHMAL		F6k	1294-1712
TGE-b superfamily recentor type I (ALK-1) (SRK3)	L17075	F6I	814-1077
	J03241	F6m	
THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY	L36052; [L36051; U11025]		
STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE		Gen	1416.1833
GROWTH AND DEVELOPMENT FACTOR) (IMBUF) (THPO)	K03000	F7a	338-595
	XXXXX	E7h	2308-2575
WTH FACTOR-BETA	AU2012	F7.	233-527
CD27 (CD70 ANTIGEN)	1,00769	F7d	627-1019
CD30	103733	270	963, 1977
CD40	LU/414	L/0	000-15//

TABLE 3 (CONT)

	GenBank #	Array Coordinate Position	Position
SETA CHAIN [Interferon gamma	U05875	F7f	1702-2039
INTERFERON REGULATORY FACTOR [Interferon regulatory factor 1] X14454	(14454	F7g	478-695
ENSUS SEQUENCE BINDING PROTEIN [DNA-	M91196	F7h	1253-1475
Hulen- ALPHA -REC [INTERFERON ALPHA-BETA RECEPTOR	J03171	F7i	2562-2740
ALPHA-BETA RECEPTOR BETA CHAIN	X77722	F7j	553-1012
AA RECEPTOR ALPHA CHAIN	J03143	F7I	66-317
INTERFERON-GAMMA HECEPTOR	X72755	L L	2021-2246
MA INDICED PROTEIN	X02530	F7n	280-613
HOUSEKEEPING GENES			
		-	

Apoptosis Array

5

In the apoptosis array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with apoptosis, e.g. cell cycle genes. In a specific apoptosis array of interest, the spots are as provided in Table 4.

TABLE 4

Cell Cycle CELL DIV COCLIN-I CYCLIN-I CYCLIN-I CYCLIN-I CYCLIN-I CYCLIN-I CYCLIN-I CYCLIN-I COC256; SERINE/ SERINE/ SERINE/ SERINE/ SERINE/ COCCIN CYCLIN			Array Coordinate
3 3 3 3 3 3 3 4 4 4 4 4 1 1 1 1 1 1 1 1		Cell Cycle - Gene Name	Alla) coolamac
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1) (P34 PROTEIN	38
3 3 3 3 3 3 4 4 4 4 4 1 1 1 1 1 1 1 1 1		KINASE) (CYCLIN-DEPENDENI KINASE 1) (CDK1)	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1) (P33 PROTEIN KINASE)	30
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1).	30
; [S78187] 5. [S78187] 8. [M64349] 9. [M64349] 9. [M90813]	M14505	CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1) (PSK-J3)	3E
; [S78187] 5; [S78187] 8 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1) (TAU PROTEIN KINASE II	
S [S78187] 3 3 3 3 3 3 4 [M64349] 5 [M64349] 6 7 7	X66364	CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE).	3F
S S S S S S S S S S S S S S S S S S S	X66365	CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1) (KINASE PLSTIRE)	36
3 3 5 5 6 7 8 8 8 8 8 8 8 [M64349] 9 9 9 7 7		CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1) (CDK-ACTIVATING KINASE) (CAK)	
1; [S78187] 5; [S78187] 5 6 7 7 8; [M64349] 8; [M64349] 9 [M90813]	120320	(39 KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1).	ЗН
3 3 3 3 3 4 4 4 4 4 4 4 1 1 1 1 1 1 1 1		CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P39I PRECURSOR (CDK5	
1; [S78187] 5 5 5 8 8 8 8 11 11 11 11 11 11 11 12 13 13 13 14 14 14 14 14 14 14 14 14 14 14 14 14		ACTIVATOR) (P39I).	3.1
[S78187] [M64349] [M90813]		CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR)	
[S78187] [M64349] [M90813]		(TAU PROTEIN KINASE II 23 KD SUBUNIT) (TPKII REGULATORY SUBUNIT) (P23)	-
[S78187] [M64349] [M90813]	X80343	(P25) (P35).	30
[S78187] [M64349] [M90813]	M81933	CDC25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48)	3K
[M64349]	M81034-[S78187]	CDC25R: M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). (CDC25HU2)	3L
[M64349]	M34065	CDC25C: M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).	ЭМ
[M64349]	CCCCC	C K - 1	3N
[M64349]	777677		30
[M64349]	1 282 10	OLIV?	48
[M64349]	022621	DEN'S	4C
[M64349]	X66358	SEKINE/IHKEONINE-PROTEIN NINAGE NINAENE	AD
[M64349]	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	75
[M64349]	X66360	SERINE/THREONINE-PROTEIN KINASE PCI AIRE-2	46.
[M64349]	X66362	SERINE/THREONINE PROTEIN KINASE PCTAIRE-3	4 L
CDC2-R CDC2-R CDC2-R CYCLIN C	L25676	SERINE/THREONINE PROTEIN KINASE PITALRE	24
CDC2-R CYCLIN C	M80629	CDC2-RELATED PROTEIN KINASE CHED	41
CYCLIN C	L33264	CDC2-RELATED KINASE PISSLRE	41
CYCLIN CYCLIN	X51688	CYCLIN A	40
CYCLIN CYCLIN M90813 CYCLIN C	M25753		4K
M90813 CYCLIN M90813 CYCLIN CYCLIN CYCLIN	M74091		4L
M90813 CYCLIN CYCLIN CYCLIN	X59798: [M64349]		4M
CYCLIN	D13639 [M90813]		4N
CYCLIN	M92287		40
	M73812		58
CYCLIN	1147413 [1 49504]		5C

TABLE 4 (CONT)

		Array Coordinate
SonBank #	Cell Cycle - Gene Name	And Control
CIDAIN #		00
147414 [L4950b]	OTCLIN UZ	5E
111791 [U12685]	CYCLIN DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION	
	ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP 1)	5F
J09579; [L25610]	(WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAPZO)	
•	CYCLIN-DEPENDENT KINASE INHIBITION TO (OTOLIN-DET LINDENT TILL STORT	5G
J22398	INHIBITOR PS/) (P3/NIP2)	
	A MILITIDIE TIMOR SUPPRESSOR 1) (MTS1). (CDKN2A)	12H
27211	CYCLINITED FINE (MULTIPLE OF INTERPRETATION OF THE STATE	
117075-11 368441	TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B).	201
1140343- [120498]	CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).	
	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MALL (HINGELLING	
		5K
X92669; [X87843]	(MNA11) (MA11) (CAP33).	51.
U10564	WEE1-LIKE PHOLEIN KINASE (EC 2.7.1.1.12) (NEE1-LIKE PHOLEIN KINASE DI K (EC 9 7 1.) (PLK-1) (STPK13)	5M
U01038	SERINE/THREONINE-PHOLEIN NILVAGE I EN (EG ETT.)	SN
U38545	PHOSPHOLIPASE U1	50
D63878	NEDDS PROTEIN HOMOLOG.	68
S72008	CDC10 PROTEIN HOMOLOG	90
U00001	CDC27HS PHOLEIN	Q9
L22005	UBIQUITIN-CONJUGALING ENCIME EX-COOST	6E
U18291	CDC16HS.	6F
U63131	CDC37 HOMOLOG.	99
U77949	CDC6-RELATED PROTEIN ATEN KINASE 1 (EC 2.7.1) (ERK1) (INSULIN-	
	EXTRACELLULAR SIGNAL-RECORD LES (MAPK 1) (P44-ERK1) (ERT2) (P44-ERK1) (ERT2) (P44-	<u>.</u>
X60188	MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE).	Π.
	EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.7) (ET I.C.) (ENTRACELLULAR SIGNAL-REGULATED KINASE 2) (MAPK 2) (P42-MAPK) (ERT1).	19
M84489	ACTIVATED PHOLEIN KINASE 2) (MAI - SEGULATED KINASE 3 (EC 2.7.1) (ERK3) (MAP	
	KINASE ISOEONM P97) (P97-MAPK).	(6)
X8009Z	EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1) (ERK4) (MAP	, ek
X59727	KINASE ISOFORM P63) (P63-MAPK).	
	EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1.7) (E111.3) (E111.3)	- Per
U25278	(BMK) KINASE	

TABLE 4 (CONT)

		Array Coordinate
GenBank #	Cell Cycle - Gene Name	Washington Washington
:	EXTRACELLIL AB SIGNAL-BEGLI ATED KINASE 6 (EC 2.7.1) (ENNS) (ENNS)	
X79483	EXTRACELLULATION OF INTERPRETATION KINASE P38 (EC 2.7.1) (MAP KINASE P38)	
	MITOGEN-ACTIVATED THE PARTITURE AMMATORY DRUG BINDING PROTEIN)	
	(CY LOKINE SUPPRESSION CONTROL OF THE SUPPRESSION O	
	(CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING TOOTEIN E) ("""	NG
1 352531 [135263]	KINASE MXI2).	
במבים (במבים	STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1) (C-JUN N-1 EHMINAL	C
1 26318	KINASE 1) (JNK-46)	
	STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1) (C-JUN IN-LENWINAL	78
1 21051	KINASE 2) (JNK-55).	
121321	STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1) (G-JUN N-1 EHMINAL	20
1134819: [1]07620]	KINASE 3) (JNK3) (MAP KINASE P49 3F12).	
	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 (EV 2.7.1.7.)	7D
U25265	(MAP KINASE KINASE 5) (MAPKK 5) (MAPKK 5) (MAPKK 1):	
	DUAL SPECIFICITY MITOGEN-ACTIVATED THO KINASE WAS TO MAPKIFIK	
	(MAP KINASE KINASE 1) (MAPKK 1) (EHK ACHVALOR NIMASE 1) ("" 1)	7E
1 05624	KINASE 1) (MEK1).	
	DUAL SPECIFICITY MITOGEN-ACTIVATED PHOLEIN KINASE MINASE (LO 2.7.1.)	7.5
1139657	(MAP KINASE KINASE 6) (MAPKK 6) (MAPKEHR RINASE 0) (OF 1809)	76
1178876	MEK KINASE 3	HZ.
M15796-[.104718]	PCNA (CYCLIN)	71
1110070 100 101 101 101 101 101 101 101		
0480/0	RETINORI ASTOMA-ASSOCIATED PROTEIN (RETINOBLASTOMA	<u>-</u>
		ر/
M15400	SUSCEPTIBILITY	7K
X74594	RB2/P130	7L
X74262	RBA/P48	7M
S66431	RBP2 RETINOBLASTIONA BINDING FILE IN	NZ.
S57153; S57160		70
X85133	RBQ1 RE INOPLASTOWA BINDING FILOTEIN	88
X85134		28
M96577	E2F-1 PRB-BINDING PROTEIN	8D
Y10479	E2F-3	H80
1115642	E2F-5	ш
1 23959	E2F-RELATED TRANSCRIPTION FACTOR (DP-1)	0
1118422	DP2 (HUMDP2), DIMERIZATION PARTNER OF E2F	
U23435; U31089	ABL INTERACTOR 2 (ABI-2) + ABL BINDING PROTEIN 3 (ABLER 3) (ANGEL ID)	5 8
L29511	GRB2 GROWTH FACTOR RECEPTOR-BOOND FROTEIN 2	

TABLE 4 (CONT)

ConBonk #	Call Cycle - Gene Name	Array Coordinate
	GRB-IR / GRB10	188
	BAE ONCOGENE	8K
	RAF R-	
	TRANSCRIPTION FACTOR AP-1 (C-JUN PROTO ONCOGENE)	M8
6	1	NB
X56681	TRANSCRIPTION FACTOR JUN-D	80
M13228	N-MYC	98
D89667	C-MYC BINDING PROTEIN	26
	NUCLEOSIDE DIPHOSPHATE KINASE B (C-MYC TRANSCRIPTION FACTOR	
L16785	(PUF)]	ЭD
X16416 [M14752]	c-abl	36
	p53 PATHWAY	
M14694	CELLULAR TUMOR ANTIGEN P53	9F
	MDM2 PROTEIN (P53-ASSOCIATED PROTEIN) + MDM2-A (GB: U33199) + MDM2-C	
212020	(GB: U33201)	96
AF007111	MDM2-LIKE P53-BINDING PROTEIN (MDMX)	H6
	P73, A MONOALLELICALLY EXPRESSED P53-RELATED PROTEIN	91
AF010311	P53 INDUCED PROTEIN	91
AF010309	PIG3 (PIG3)	9K
AF010312	PIG7 (PIG7)	J6
	PIG10 (PIG10)	Ме
	PIG11 (PIG11)	N6
	PIG12 (PIG12)	06
U90313	GLUTATHIONE-S-TRANSFERASE HOMOLOG	10B
U66469	P53-DEPENDENT CELL GROWTH REGULATOR CGR19	10C
AF001954	GROWTH INHIBITOR P33ING1 (ING1)	10D
L13698	GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1).	10E
	BCL FAMILY	
M14745	BCL2	10F
U58334	BCL2 AND P53 BINDING PROTEIN BBP/53BP2 (BBP/53BP2)	10G
L22474	ВАХ	10H
U59747	APOPTOSIS REGULATOR BCL-W	101
1.08246	INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL-1 (ORF IS AT NT. 61-1053: ML)	103
21 1201		

TABLE 4 (CONT)

		40117
		Array Coordinate
GenBank #	OTEIN) (HEMOPOIETIC-SPECIFIC EARLY	10K
199680		10L
2		10M
1123765; [U16812; U		10N
1		100
066879	ECEPTOR-	9
593171-[735491]		110
U76376	Harakiri, a protein that activates cell death and Interacts w. Dore and con-	
	CASPASE CASCADE	
	CASPASES ***** CASPASES *****	11D
113699 [M87507; X	113699- M87507; XG(ICE) (INTERLEUKIN-1 BETA CONVEH IING ENZ I MIL) (1 43) (2)	11E
U13021; [U13022]	(CASPASE-2) (ICH-1L) (ICH-1S) APOPAIN PRECURSOR (EC 3.4.22) (CYSTEINE PROTEASE CPP32) (YAMA PROPAIN PRECURSOR) (CASPASE-3) ISOFORM	
	PROTEIN) (CASPASE-3) (CPP32) (TAMATING TENT) (CASPASE-3)	11F
U13737	ALPHA ICH-2 PROTEASE PRECURSOR (EC 3.4.22) (TX PROTEASE) (ICEREL-II) ICASPASE-4) + CASPASE-5 PRECURSOR (EC 3.4.22) (ICH-3 PROTEASE) (TY	11G
J28014; U28015	PROTEASE (ICEREL-III).	
1120537: U20536	ISOFORM BETA + ISOFORM ALPHA	
05020,	CASPASE-7 PRECURSOR (EC 3.4.22) (ICE-LINE AL CITICAL) (CASPASE-7 PRECURSOR (EC 3.4.22) (ICE-LINE AL CITICAL)	111
U37448	CASPASE-8 PRECURSOR (EC 3.4.22) (ICE-LIKE APOPTOTIC PROTEASE 5)	
	(MORTI-ASSOCIATED CED-3 POWCECO) (MINIORY) (APOPTOTIC CYSTEINE ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE)	117
U60520; U58143; >	U60520; U58143; X98PROTEASE, (APOPTOTIC PHOTEASE MOTES) (CE-LIKE APOPTOTIC PROTEASE 5) CASPASE-8 PRECURSOR (EC 3.4.22) (ICE-LIKE APOPTOTIC PROTEASE 5)	
	(MORT1-ASSOCIATED CED-3 HOMOLOGY) (W. FLICE) (APOPTOTIC CYSTEINE ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (APOPTOTIC CYSTEINE ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE)	11K
U60520; U58143; 3	U60520; U58143; X98 PROTEASE) (APOPTOTIC PROTEASE MUH-5) (UAT4) (CAT4) (CATA (CASPASE 6) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LIKE APOPTOTIC PROTEASE 6)	1
U56390; [U60521]	LAP6) (APOPTOTIC PROTEASE MCH-6) ICE-LIKE APOPTOTIC PROTEASE 4 PRECURSOR (EC 3.4.22) (APOPTOTIC	11M
U60519	PROTEASE MCH-4) (CASPASE-10)	

TABLE 4 (CONT)

		Array Coordinate
GenBank #	Cell Cycle - Gene Name	
		24
41690	D PROTEIN (TRADD)	110
		12B
J78798; [L81153]	TRAF6	
,		12C
U59863; [U53830]	PROTEIN (TRIP)	12D
	SERINE/THREONINE PROTEIN KINASE, NIK; BINDS SPECIFICALLY 10 I RAFZ	125
110200	CASPER, A FADD. AND CASPASE-RELATED INDUCER OF APOPTOSIS [CASH-	12F
AF010127[Y14039; Y	AF010127[Y14039; Y ALPHA+ CASH-BETA] (FLAME-1) (FLAME-1) AF010127[Y14039; Y ALPHA+ CASH-BETA] (FLAME-1) (FLAME-1) (FLAME-1) AF010127[Y14039; Y ALPHA+ CASH-BETA] (FLAME-1) (FLAM	
	Щ	12G
U84388	RIP	12H
J50062]	CELL DEATH PHOTEIN MINASE THE ACTIVATES JNK AND APOPTOSIS	121
AF015956	DAXX, A FAS-BINDING TO TAPE 2 RECEPTOR ASSOCIATED PROTEIN (TRAP3) TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN (TRAP3)	12.1
U12597	CAP-1) (IMP1 ASSOCIATED	
	CD40 RECEPTOR ASSOCIATED PACTOR (CIPALITY COME)	12K
U21092; [U15637; L34PHO1EIN]	INHIBITOR OF APOPTOSIS PROTEIN 1 (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF	101
U45878; [U37546]	SIGNALLING COMPLEX PROTEIN 1) (IAP HOMOLOG C) (IAP 1) (MINO).	771
	INHIBITOR OF APOPTOSIS PROTEIN 2 (HIAP2) (HIAP-2) (CTAT-1) (TWO TO THE PROTEIN 2) (IAP HOMOLOG B) (IAP2) (MIHB).	12M
U45879; [U37547]	SIGNALLING COMPLEX TOOL FINE STANDING IN (IAP-X-LINKED INHIBITOR OF APOPTOSIS PROTEIN (X-LINKED IAP)	Not
U45880; [U32974]	LIKEPROTEIN) (HILP).	
		Cot
X01394	TUMOR NECROSIS FACTOR [TNF-a]	021
	MPHOTOXIN-ALPHA [FORMERLY LUMOR INECHOSIS FACTOR DETAIN	14B
D12614	D)]	14C
L11015	THE ALBHA CONVERTING ENZYME	14D
069611	FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) (APT1LG1) (FASL)	14E
D38122; [U08137]	APO 3116 AND (TNE-BEI ATED APOPTOSIS INDUCING LIGAND TRAIL)	14F
057059	AFO-2 LIGARID (III)	

TABLE 4 (CONT)

		Array Coordinate
GenBank #	Cell Cycle - Gene Name	Airay Cool dinate
	SECRETED APOPTOSIS RELATED PROTEIN 1	24-
	SECRETED APOPTOSIS RELATED PROTEIN 3 (SARP3)	14H
	TUMOR NECROSIS FACTOR RECEPTOR TUMOR NECROSIS FACTOR DECEPTOR 1 (55KN)	15B
M33294	TUMOR NECROSIS FACTOR RECEPTOR TUMOR NECROSIS FACTOR	()
M32315	RECEPTOR 2]	190
Z70519	FAS/APO 1	150
U90875	CYTOTOXIC LIGAND TRAIL RECEPTOR	100
AF016268	HECEPTOR 5 (DR5)	LC.
Y09392; [U75380;U74WSL-L		501
M27544	IN-LIKE GROWTH FACTOR IA	157
M29645	INSULIN-LIKE GROWTH FACTOR II (Somatomedin A)	100
X04434	N-LIKE GROWTH FACTOR I RECEPTOR	16C
	CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR [insuline-like	!
V00285- [J03528]	growth factor receptor II, IGFR-2]	160
D25216	IGFBP COMPLEX ACID LABILE CHAIN	16E
M25/10	IGEBP2	16F
0140011	IGFBP3 (GROWTH HORMONE-DEPENDENT INSULIN-LIKE GROWTH FACTOR-	
M31159: [M35878]	BINDING PROTEIN)	16G
M62403	IGFBP4	16H
M65062	IGFBP5	17B
MESANS	IGFRP6	17C
MUCHOC		
	OTHER REGULATORS	
	DEATH-ASSOCIATED PROTEIN 3 (DAP-3) (ionizing radiation resistance conferring	1
U18321; [X83544]	protein)	U/-
X76104	DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1) (DAP KINASE 1).	1/E
X86779	Fas-activated serine/threonine kinase (FAS1) phosphorylates 11A-1	1/L
S78085	PDCD2	5/1
M63167	Akt1 (rac protein kinase alpha, protein kinase B, c-Akt)	17H
M77198: [M95936]	AKT2 (rac protein kinase beta)	18B
1163295	seven in absentia homolog	18C
1137688	BATS1	18D
1191985	DNA fragmentation factor-45	18E
AE022385	apoptosis-related protein TFAR15 (TFAR15)	18F
1156976	calmodulin dependent phosphodiesterase PDE1B1	18G
2 1222		

TABLE 4 (CONT)

		Array Coordinate
GenBank #	Cell Cycle - Gene Name	Allay cooldinate
1182038	CD27BP (Siva)	181
100000	Appropriate segmentation gene homolog CAS	19B
033200	Cilibration order of the community of the city of the	19C
075285	apopilosis iriilibiiloi sui viviii	19D
L25080		100
L09210	NITRIC OXIDE SYNTHASE (2A,INDUCIBLE)	
M58603	NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT	TP.
M83221	TRANSCRIPTION FACTOR RELB [I-Rei]	19G
108015	NF-ATc (Transcription factor (NFATc.b)]	20B
D15057	DAD-1 (DEFENDER AGAINST CELL DEATH 1)	20C
	ERI	1
M74816	apolipoprotein J; sulfated glycoprotein-2]	20D
D13889	DNA-BINDING PROTEIN INHIBITOR ID-1	20E
V15722		20F
100746	ASE MICH	20G
100/40	GLUTATHIONE S-TRANSFERASE M4 [GLUTATHIONE S-TRANSFERASE MU 1]	
YORUSU		218
V45400	CLITATHIONE S.TRANSFERASE P	21C
710400		
M14777	subunit 1]	210
M01304	GIUTATHIONE PEROXIDASE	21E
V70200	GI ITHATHIONE S-TRANSFERASE (THETA 1)	21F
17,300	NADDH, CYTOCHROME P450 REDUCTASE	21G
290409	CROWTH ABREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-	
C40706 [CE2138]	DAMAGE INDICIBLE PROTEIN) (CHOP).	22B
240100100000	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (DNA-	
M60974	DAMAGE INDUCIBLE TRANSCRIPT 1) (DDIT1).	220
U15172	NiP1	ZZD
115174	NIP3	22E
1 07414	CD40 LIGAND	22F
1.08096	CD27 LIGAND CD70 antigen1	22G
VOCESE	SOTEIN	23B
Vacabot	RETINOIC ACID RECEPTOR RXR-BETA	23C
M04020	RETINOIC ACID RECEPTOR BETA-2	23D
AU/ 202	PROTEIN.TYROSINE PHOSPHATASE ZETA	23E
M93420	EVOICION REPAIR PROTEIN FRCC6	23F
L04/91	EAUSION THE AND THE PRINCIPLE OF THE PRI	

TABLE 4 (CONT)

		Array Coordinate
GenBank #	Cell Cycle - Gene Name UV EXCISION REPAIR PROTEIN PROTEIN RAD23 [xeroderma pigmentosum group	23G
021090	C repair complementing protein poornringous	
	LOUISEKEEPING GENES	
	TOODEN THE CHILD	1A
M26880	UBICUITIN	18
M86400	PHOSPHOLIPASE AZ	10
V00530	HYPOXANI HINE-GOANING TITIOGI TO THOUSE THE DEHYDROGENASE	10
X01677	GLYCERALDEHYDE 3-PHOSPITALL DEILIGICGER	1
K00558	TUBULIN ALPHA	4
M11886	HLA CLASS I HISTOCOMPA I IBILLI I ANTIGEN, O-7 ALL INC.	16
X00351	BETA-ACTIN	1H
X56932	23 KD HIGHLY BASIC PROTEIN	-
1114971	RIBOSOMAL PROTEIN S9	
	NEGATIVE CONTROLS	
	M13 mp18(+) STRAND DNA	Z 7
	-DNA	7-
	ol C 18	1
		1M1N101P
	CALIBRATION MARKERS	
	OBJENTATION MARKERS	20000 12M3A3D6A6P9A9P12A12
		ACCOUNT IS TO
	Dark spuis	2A2B2C2E2F2HZIZKZLZNZOZF4/
	Faint spots	
	Column 13 is Diank	

Human Stress Array

5

In the human stress array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with stress responses of human cells, e.g. stress response regulators and effectors. In a specific human stress array of interest, the spots are as provided in Table 5.

TABLE 5

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
K00650	C-fos
M31630	CAMP RESPONSE ELEMENT BINDING PROTEIN CRE-BYT. (CAMP responsive agricum) binding protein 1)
M34356	CREB (ACTIVE TRANSCRIPTION FACTOR)
x60188	EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1) (ERK1) (INSULIN- SIIMULALED) MAP2 KINASE) (MAP KINASE 1) (MAPK 1) (P44-ERK1) (ERT2) (P44-MAPK) (MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE).
M84489	EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAPK 2) (P42-MAPK) (ERT1).
X80692	EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1) (ERK3) (MAP KINASE ISOFORM P97) (P97-MAPK).
X59727; S38873	EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1) (EKK4) (MAP' KINASE ISOFORM P63) (P63-MAPK).
U25278	EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC. 2.7.1) (EKKS) (EIKK4) (BIVIN 1 NII VAAL).
X79483 U53442	EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1) (ERK6) (ERK5). MITOGEN-ACTIVATED PROTEIN KINASE P38 BETA (EC 2.7.1) (MAP KINASE P38 BETA).
126318	STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1) (C-JUN N-TERMINAL KINASE 1) (JNK 46)
131951	STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1) (C-JUN N-TERMINAL KINASE 2) (JNK 55).
U25265; (U71087; U71088)	U25265; (U71087; DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1)(MAP U71088) KINASE KINASE 5) (MAPKK 5) (MAPK/ERK KINASE 5) (MEK5)
	MAP KINASE KINASE MEK5B. MAP KINASE KINASE MEK5C

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTIONS STRESS RESPONSE REGULATORS AND EFFECTIONS (MAP
105624	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN WILL SPECIFICITY MINASE 1) (MAPK/ERK KINASE) (MEK1). KINASE KINASE 1) (MAPK/ERK KINASE)
111285	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (EC 2.7.1)(MAPKINASE KINASE 2) (MAPKK 2) (ERK ACTIVATOR KINASE 2) (MAPK/ERK KINASE) (MEK2).
U39657	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 6 (EC 2.7.1)(MAPKINASE KINASE 6) (MAPKK 6) (MAPK/ERK KINASE 6) (SAPKK3).
U78876	MEK KINASE 3 STE20-LIKE KINASE OXIDANT STRESS KINASE (YSK1, STE20 and SPS1 RELATED KINASE)
U77129	SPS1/STE20 HOMOLOGUE, KHS, ACTIVATOR OFJUN N-TERMINAL KINASE (HSU77129)
U07349 1166464	B LYMPHOCYTE GERMINAL CENTER KINASE (HSU07349) HEMATOPOIETIC PROGENITOR KINASE ACTIVATOR OF SAPK/JNK (HPK1) (HSU66464)
AB005216 X17576	NCK, ASH AND PHOSHPHOLIPASE C GAMMA-BINDING PROTIEN NAP4(AB005216) NCK MELANOMA CYTOPLASMIC SRC HOMOLOGUE (HSNCK)
U24153	SERINE/THREONINE-PROTEIN KINASE PAK-GAMIMA (EC 2.7.1) (GAMIMA-PAK) (P21-ACTIVATED KINASE 3) (PAK65) (S6/H4 KINASE) (PAK2) PAK3.
M35543	G25K GTP-BINDING PROTEIN, BRAIN ISOFORM (GP) (CDC42 HOMOLOG) CDC42. THIMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN(TRAP1)(HSU12595)
012595	TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN(TRAP2) (HSU12596)
X17620	NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (NDP KINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR NM23)
F	(NIM23-H1). LEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR 1)(HSTF
M646/3	1). HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF 2) (HSF 2) (HSF 2) (HSTF 2) (HSF 3) (H
D87673	12). HEAT SHOCK TRANSCRIPTION FACTOR 4. HEAT SHOCK TRANSCRIPTION FACTOR 4.
134075	FKBP-RAPAMYCIN ASSOCIATED TROTEIN ASSOCIATED TROTEI

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
M35663; (U50648)	INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE (P68 KINASE)
-	10 KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONIN)
D86956	HEAT-SHOCK PROTEIN 110 KD (KIAA0201)
X54079:	HEAT SHOCK 27 KD PROTEIN (HSP 27)(STRESS-RESPONSIVE PROTEIN
.139370;	27)(SRP27)(ESTROGEN-REGULATED 24 KD PROTEIN) (28 KD HEAT SHOCK PROTEIN).
X16477; Z23090;	
X61598; D83174	47 KD HEAT SHOCK PROTEIN PRECURSOR (COLLAGEN-BINDING PROTEIN 1) (COLLIGIN
	C
M11717; (M59828)	(M59828) HEAT SHOCK 70 KD PROTEIN 1 (HSP70-1) (HSP70-1/HSP70-2).
	(9) OF WOODER IN STATEM OF THE RUCKY TO VIO BROTEIN 9)
126336	HEAT SHOCK-RELATED YORD PROTEIN 2 (HEAT SHOCK YORD TWO LET'S 2).
L12/23	HEAT SHOCK 70 KD PROTEIN 4 (15) 2017. HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
	HEAT SHOCK 70 KD PROTEIN 7 (HEAT SHOCK 70 KD PROTEIN B) (FRAGMENT).
Y00371	HEAT SHOCK COGNATE 71 KD PROTEIN.
X07270; (X15183;	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86).
M27024; M30626;	
M30627)	VO dollar and dollar and do dollar
M16660 U15590	HEAT SHOCK PROTEIN HSP 90-BEIA (HSP 84) (HSP 90) HEAT SHOCK PROTEIN 27 (heart)
020243	HEAT SHOCK PROTEIN HSP72 HOMOLOG (FRAGMENT).
U40992	HEAT SHOCK PROTEIN HSP40HEAT SHOCK PROTEIN HSP40 HOMOLOG.
15189	REGULATED PROTEIN) (GRP 75) (PEPTIDE-BINDING PROTEIN 74) (PBP 74) (MORTALIN) (MOD).
U28918	HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN)
D13388	DNAJ PROTEIN HOMOLOG 2 (DNAJ2 OR HDJ2)
D49547; (D17749)	
M19645	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN RINDING PROTEIN) (BIP)

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
L10284; (L18887; M94859: M984521	CALNEXIN PRECURSOR (MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ANTIGEN- BINDING PROTEIN P88) (P90) (IP90)
	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)(52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A)
305016	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72)
124804; (124805)	P23 PROGESTERONE RECEPTOR ASSOCIATED PROTEIN (HUMPRA)
M86752	transformation -sensitive protein (ief SSP 3521)
111667	CYCLOPHILIN-40
U73704	48 kDa FKBP-ASSOCIATED PROTEIN FAP48
U42031	54 KDA PROGESTERONE RECEPTOR-ASSOCIATED PROTEIN FKBP54
M34539; (M80199;	M34539; (M80199; FK506-BINDING PROTEIN (FKBP) (FKBP12) (PEPIIDYL-PROLYL CIS-IRANS ISOMERASE)
M80706;M92423;	(PPIASE) (ROTAMASE)
x52220)	
M88279	IMMUNOPHILUN (FKBP52)
M65128	RAPAMYCIN-BINDING PROTEIN (FKBP-13)
X56134 (M14144;	VIMENTIN, INTERMEDIATE FILAMENT PROTEIN
(pcc617	(NGPL) (NETCORE EVALUATION OF A CORP. CARROLL STREET OF A STREET
M34664; (M22382)	M34664; (M22382) MITOCHONDRIAL MATRIX PROTEIN PT PRECURSOR (POLYMPHOCYTE PROTEIN) (INSPUT) OR HSP60) (CHAPERONIN HOMOLOG) (HUCHA60) (HEAT SHOCK PROTEIN 60)
\$83171; (235491)	BCL-2 BINDING ATHANOGENE-1 (BAG-1) (GLUCOCORTICOID RECEPTOR-ASSOCIATED BADAS)
023662	LIBIQUITIN-LIKE PROTEIN (NEDD8)
X52882	1-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)(CCT-ALPHA) CCT1 OR CCTA OR
U38846	1-COMPLEX PROTEIN 1, DELTA SUBUNIT (TCP-1-DELTA)(CCT-DELTA) (STIMULATOR OF TAR RNA BINDING) (HSU38846).
	MOLOWIN (U) MICHAEL TOOMON TO THE TOTAL CHORLES AND
D43950	1-COMPLEX PROJEIN 1, EPSILON SUBUNII (ICP-1-EPSILON)(CC1-EPSILON) (HUMING IDD)
X74801; (U17104)	X74801; (U17104) T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA)(CCT-GAMMA) (CCT3) OR (CCTG) OR (TRIC5) (HSHUMAPC).

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
U83843	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)(HIV-1 NEF INTERACTING
013497	PROJEIN (138828-43). T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)(CCT-THETA) (HUMRSC548).
	HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) (HSOXYGR).
(\$34389)	HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2)
	ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULAIED PROTEIN)(GRA74) (GR794) (HOMOLOG) (TUMOR REJECTION ANTIGEN 1) (HSTRA1).
005569	ALPHA CRYSTALLIN A CHAIN (HSU05569).
\$45630	ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN) (ROSENTHAL HBEK COMPONENT).
U59058	BETA CRYSTALLIN A3 (HSU59058).
U59057	BETA CRYSTALLIN A4 (HSU59057).
U35340	BETA CRYSTALLIN B1 (CRYBB1) (HSU3534U).
110035	BETA CRYSTALLIN B2 (BP) (HUMCRYB2B).
U71216	BETA CRYSTALLIN B3 (9CRYBB3 OR CRYB3) (H3U/1210).
136869	BETA CRYSTALLIN S (GAMMA CIRYSTALLIN 3) (CIRYGS) OIR (GIRTGO).
U66582: M11971;	GAMMA CRYSTALLIN C (GAMMA CRYSTALLIN 2 OR 1/3) (CRYGC) OR (CRYG3).
(M11970)	
	GAMMA CRYSTALLIN B (GAMMA CRYSTALLIN 1-2) (CRYGG) OR (CRTG2) (HUMCRYGX1).
102950	MU-CRYSTALLIN HOMOLOG (CRYM) (HUMMUCRYS).
113278; (\$58039)	QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE KEDUCTASE) (ZELATORYSTALLIN).
D16234; (Z49835;	PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60)
D83485; U42068)	(58KDA MICROSOMAL PROTEIN) (phospitolipase C-ulping)
D49489	PROJEIN DISOLFTIDE ISOLVILINATE OF TAKE EACTOR OF IRINIT 1 (FPET) (R3-1) (C11 PROJEIN)
M75715	EUKARYOTIC PEPIIDE CHAIN KELEASE FACTOR SOBOTATION OF THE STATES TO THE
D49490	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (EC 5.3.4.1) (PDIR) (HUMPDIR).
J02783; (X05130;X07077)	
	(P55)(HSPRO4HY).

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
	Glutathione-insulin transhydrogenase (EC 5.3.4.1 /1.8.4.2); protein-disulfide reductase (all tathione) (HSGIIR).
M86737	STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 (SSRP1) (RECOMBINATION SIGNAL SEQUENCE RECOGNITION PROTEIN) (1160) SSRP1.
X63368; (S37374; 1	DNAJ PROTEIN HOMOLOGS HSJ1A protein; HSJ1B protein.(HSJ-1)(HSHSJ1MR)
	150 KDA OXYGEN-REGULATED PROTEIN ORP 150 (HSU65785)
	DNA DAMAGE RESPONSE/REPAIR/RECOMBINATION
X90392 : (L40817;	MUSCLE-SPECIFIC DNASE I-LIKE (DNasø X) (XIB)
	RAD
M96684	TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA
M29971	METHYLATED-DNAPROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (MGMT)
U09579; (L25610)	CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1) (WAF1) (CDKN1A) (CDKN1) (SD11) (PIC1) (CAP20)
L37374	FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) (FEN-1)
U70310	DNA REPAIR PROTEIN XRCC9
HT3218 (X02317;	SUPEROXIDE DISMUTASE (CU-ZN) (EC 1.15.1.1) SOD1.
K00065)	(UCS-C3) (1 1 St 1 C3) (NC 1 C) (C) INC (C) (C) (C) (C) (C) (C) (C) (C) (C) (C
J02947	EXTRACELLULAR SUPEROXIDE DISMUIASE PRECORSOR (CU-213) (EC 1.10.11.) (CC-30.0). SOD3.
X07834; (X59445)	SUPEROXIDE DISMUTASE PRECURSOR (MN) (EC 1.15.1.1) SOD2
M14694; (M14695)	M14694; (M14695) CELLULAR TUMOR ANTIGEN P53
Z12020; (M92424)	MDM2 PROTEIN (P53-ASSOCIATED PROTEIN)
	MDM2-A (GB: U33199)
	MDM2-C (GB: U33201)
U33841	ATAXIA TELANGIECTASIA (ATM)
J03250	DNA TOPOISOMERASE I (TOP1)
J04088	DNA TOPOISOMERASE II, ALPHA (TOP2A)
X68060	DNA TOPOISOMERASE II, BETA (TOP2B)
U43431	DNA TOPOISOMERASE III (TOP3)

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
S40706 (S62138)	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD 153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP)
X04076 X51420	CATALASE (EC 1.11.1.6) CAT. 5.6-DIHYDROXYINDOLE-2-CARBOXYLIC ACID OXIDASE PRECURSOR (DHICA OXIDASE) (TYROSINASE-RELATED PROTEIN 1) (TRP-1) (CATALASE B) (GLYCOPROTEIN-75) (GP75)
X15453	BASE EXCISION REPAIR URACIL-DNA GLYCOSYLASE PRECURSOR (UNG.1)
X52486	URACIL-DNA GLYCOSYLASE 2 (UNG2) DNA-3 METHYLADENINE GLYCOSYLASE (3-METHYLADENINE DNA GLYCOSYLASE)
[VI/4905]	(ADPG) (3-ALKYLADENINE DNA GLYCOSYLASE) (N-METHYLPURINE-DNA GLYCOSIRASE)
U51166	G/T MISMATCH-SPECIFIC THYMINE DNA GLYCOSYLASE (TDG)
Y11838	8-OXYGUANINE DNA GLYCOSYLASE HOMOLOG 1 (mutim HOMOLOG) (UGH1) (HOGG1) (FGPYG)
U63329	muty HOMOLOG (HMYH)
X59764; (X66133)	DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE (AP ENDONUCLEASE 1) (APEX NUCLEASE) (APEN) (REF-1 PROTEIN) (APE1)
079718	ENDONUCLEASE III HOMOLOG 1 (HNTH1) (OCTS3)
M36067	DNA LIGASE I (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNL1) (LIG1)
M18112	POLY (ADP-RIBOSE) POLYMERASE (PARP) (ADPRT) (NAD (+) ADP-RIBOSYLTRANSFERASE) (POLY (ADP-RIBOSE) SYNTHETASE) (PPOL)
D16581	7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (muti HOMOMOLOG) (8-0XO-DGTPASE) (MIH1)
M36089	DNA-REPAIR PROTEIN XRCC1
M11722	DNA POLIMERASE BEINGE OF THE MAIN AND THE ADDITION ENZYME) (TERMINAL DNA NUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE) (DNT) (TD1)
X55715	40S RIBOSOMAL PROTEIN S3 (POSSIBLE dRpase) NUCLEOTIDE EXCISION REPAIR

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
D14533	DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS (XERODERMA PIGMENTOSUM GROUP A COMPLEMENTING PROTEIN)
M31899	DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA PIGMENTOSUM GROUP B COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC3) (BASAL TRANSCRIPTION FACTOR 2 89 KD SUBUNIT) (BIF2-p89) (TFIIH 89 KD SUBUNIT)
D21089	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (p.125)
D21235 D21090	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A) UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B (HHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KD PROTEIN) (p58)
X52221; (HT1175)	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2)
018299	DAMAGE-SPECIFIC DNA BINDING PROTEIN p127 SUBUNIT; IMPLICATED IN XERODERMA PIGMENTOSUM GROUP E (DDB1)
U18300	DAMAGE-SPECIFIC DNA BINDING PROTEIN p48 SUBUNIT; IMPLICATED IN XERODERMA PIGMENTOSUM GROUP E (DDB2)
177890	DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELLS (XERODERMA PIGMENTOSUM GROUP F COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-4)
L20046; (X69978)	L20046; (X69978) DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-5)
U28413	COCKAYNE SYNDROME GROUP A; WD-REPEAT PROTEIN (CSA PROTEIN)
104/91	EXCISION REPAIR PROTEIN ERCC-0 (C3B) RASIC TRANSCRIPTION FACTOR 69 KD SHIRLINIT (C69) (RTF9069)
730094	BASIC TRANSCRIPTION FACTOR 2, 44 KD SUBUNIT (BIF2P44)
Z30093	BASIC TRANSCRIPTION FACTOR 2, 34 KD SUBUNIT (BIF2p34)
Y0/595	BASIC IKANSCIKIPIION FACIOIX 2, 32 KD SUBUINI (BIT-2032) DNA FXCISION REPAIR PROTEIN FRCC-1
17.101111	

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
M63488	REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE STRANDED DNA-BINDING PROTEIN)
105249	REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2)
107493	REPLICATION PROTEIN A 14 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR A PROTEIN 3)
U24186	REPLICATION PROTEIN A 30 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 4)
M15796; (J04718)	COLIFERATING
107540	ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (RFC36) ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (RFC37)
[0754]	
M87338	_
L14922	ACTIVATOR 1 140KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD
	SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA)
X06745	DNA POLYMERASE ALPHA
M80397	DNA POLYMERASE DELTA CATALYTIC CHAIN
M60974	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD-45 (DNA-DAMAGE INDITION ICIBLE TRANSCRIPT 1) (DDIT1) (GA45)
\$40706 (\$62138)	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD 153 (DNA-DAMAGE)
	Homologous recombination
U63139	DNA REPAIR PROTEIN RAD50
D13804; (D14134)	DNA REPAIR PROTEIN RAD51 HOMOLOG
012134	
009820	X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP) (RADS4L) (XH2)
X97795	DNA REPAIR PROTEIN RAD54 HOMOLOG
U14680	BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (BRCA1)
U43746	BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN (BRCA2)
D63882	MEIOTIC RECOMBINATION PROTEIN DMCI/LIMIS HOMOLOG
X83441	DNA LIGASE IV (POLYDEOXYRIBONDOLEOIIDE SYNIFIASE (AIP)) (DINL4)

TABLE 5 (CONT)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
M74524	HHR6A (YEAST RAD6 HOMOLOG) (UBIQITIN-CONJUGATING ENZYME) (UBCA)
	HHR6B (YEAST RAD6 HOMOLOG) (UBIQITIN-CONJUGATING ENZYME) (UBCB)
Y08837	RAD51-LIKE PROTEIN (POSSIBLE XRCC2)
	Non-homologous end-rejoining
U40622	DNA REPAIR PROTEIN XRCC4
; (538729)	ATP-DEPENDENT DNA HELICASE II, 70 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P70) (70 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTO-ANTIGEN) (TLAA) (KU70) (CTC BOX BINDING FACTOR 75 KD SUBUNIT) (CTCBF) (CTC75) (XRCC6)
M30938	ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 85 KD SUBUNIT) (CTCBF) (CTC85) (NUCLEAR FACTOR IV) (KU80) (XRCC5)
(77077)11	DALA DEDENDENT PROTEIN KINASE (DNA-PK)
- 1	DNA DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (DNA-PKCs) (XRCC7)
M29474	V(D)J RECOMBINATION ACTIVATING PROTEIN 1 (RAG 1) (RAG-1)
M94633	V(D)J RECOMBINATION ACTIVATING PROTEIN 2 (RAG2) (RAG-2)
	MISMATCH REPAIR
U07418; (U07343)	_
U04045; (L47583)	DNA MISMATCH REPAIR PROTEIN MSH2 DNA MISMATCH REPAIR PROTEIN MSH3 (DIVERGENT UPSTREAM PROTEIN) (MISMATCH
, ,	REPAIR PROTEIN 1) (MRP1) (DUP) (DUG)
U54777	DNA MISMATCH REPAIR PROTEIN MSH6 (muts - ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160)
U13696	DNA MISMATCH REPAIR PROTEIN PMS2 (PMS1 PROTEIN HOMOLOG 2)
	STATE OF STA
013095	DINA WISIWALCH KETAIK TROJEIN 1951 (TROJEIN TROJEIN TO TROJEIN TR
X14672; X17059	ARYLAMINE N-ACETYLTRANSFERASE, POLYMORPHIC (EC 2.3.1.5) (PNAT) +
	ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC (EC 2.3.1.5) (MNAT)
200036	CYTOCHROME PA50 IA2 (EC 1.14.14.1) (PA50-P3) (PA50-4):515
200036	CYTOCHROME P450 IA2 (EC 1.14.14.1) (P450-P3) (P450-4):313

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
J04449; D00003; J04813: D00408	CYTOCHROME P450 IIIA4 (EC 1.14.14.1) (NIFEDIPINE OXIDASE) (NF-25) (P450-PCN1)
	CYTOCHROME P450 IIIA3 (EC 1.14.14.1) (GLUCOCORTICOID-INDUCIBLE) (HLP) CYP3A3.
	CYTOCHROME PA50 IIIA5 (EC 1.14.14.1) (P450-PCN3)
	CYTOCHROME P450 IIIA7 (EC 1.14.14.1) (P450-HFLA)
J02871	CYTOCHROME P450 IVB1 (EC 1.14.14.1) (P450-HP)
M33318; (X13930;	M33318; (X13930; CYTOCHROME P450 IIA6 (EC 1.14.14.1) (COUMARIN 7-HYDROXYLASE) (IIA3) (P450(I))
CYTOCHROME	CYTOCHROME P450 IIA7 (EC 1.14.14.1) (P450-IIA4)
P450 IIA7 (EC	
1.14.14.1) (P450-	
M21940; M15331;	CYTOCHROME P450 IIC9 (EC 1.14.14.1) (P450 PB-1) (P450 MP-4) (S-MEPHENYTOIN 4-
(M21939)M61858; HYDROXYLASE)	HYDROXYLASE)
(L07093); M61853;	(L07093); M61853; CYTOCHROME P450 II
M61854	
009178	DIHYDROPYRIMIDINE DEHYDROGENASE (NADP+) PRECURSOR (EC 1.3.1.2) (DPD)
	(DIHYDROUKACIL DEHYDROGENASE) (DIHYDROINTININE DEHYDROGENASE) DY 10.
M64082	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL
	HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHY DAVILINE OXIDASE 1)
M83772	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.14.13.8) (HEPATIC
	FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE OXIDASE 3) (FMO II)
211737	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 4 (EC 1.14.13.8) (HEPATIC
	FLAVIN-CONTAINING MONOOXYGENASE 4) (FMO 4) (DIMETHYLANILINE OXIDASE 4)
L37080	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 5 (EC 1.14.13.8) (HEPATIC
	FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5)

Genbank #	STRESS RESPONSE REGULATORS AND EFFECTORS
GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
X04808	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE)
M14758	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
M23234	MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3)
105628	MULIIDRUG RESISTANCE-ASSOCIATED PROTEIN 1
U08021	NICOTINAMIDE N-METHYLTRANSFERASE (EC 2.1.1.1)
U09031; U28170; L19956	PHENOL-SULFAIING PHENOL SULFOIRANSFERASE 1 (EC. 2.8.2.1) (P-P31) (INERNICAI ABLE) PHENOL SULFOIRANSFERASE) (TS-PST) (HAST1/HAST2) (ST1A3) STP1 OR STP.
	PHENOL-SULFATING PHENOL SULFOTRANSFERASE 2 (EC 2.8.2.1) (P-PST) (ST1A2) STP2.
	MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (EC 2.8.2.1) (SULFOTRANSFERASE, MONOAMINE-PREFERRING) (M-PST) (THERMOLABILE PHENOL SULFOTRANSFERASE) (TL-PST) (PLACENTAL ESTROGEN SULFOTRANSFERASE) (CATECHOLAMINE-SULFATING PHENOL SULFOTRANSFERASE) (HAST3) STM.
U08854; X63359; U06641; J05428; V00317	UDP-GLUCURONOSYLTRANSFERASE 2B15 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UDPGTH-3) UGT2B15.
	UDP-GLUCURONOSYLTRANSFERASE 2810 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) UGT2810.
	UDP-GLUCURONOSYLTRANSFERASE 288 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (ESTRIOL SPECIFIC) (HLUG4) (FRAGMENT) UGT288.
	UDP-GLUCURONOSYLTRANSFERASE 2B7 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (3.4-CATECHOL ESTROGEN SPECIFIC) (UDPGTH-2) UGT2B7.
	UDP-GLUCURONOSYLTRANSFERASE 284 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPG1) (HYODEOXYCHOLIC ACID) (HLUG25) (UDPGTH-1) UGT284.

GenBank # S	STRESS RESPONSE REGULATORS AND EFFECTORS
M68840	AMINE OXIDASE (FLAVIN-CONTAINING) A (EC 1.4.3.4) (MONOAMINE OXIDASE) (MAO-A) MAOA
M69177	AMINE OXIDASE (FLAVIN-CONTAINING) B (EC 1.4.3.4) (MONOAMINE OXIDASE) (MAO-B) MAOB.
K03191	CYTOCHROME P450 IA1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE).
M29874	CYTOCHROME P450 IIB6 (EC 1.14.14.1) (PHENOBARBITAL-INDUCIBLE) (P450 IIB1).
	CYTOCHROME P450 IID6 (EC 1.14.14.1) (P450-DB1) (DEBRISOQUINE 4-HYDROXYLASE) CYP2D6.
J02625	CYTOCHROME P450 IIE1 (EC 1.14.14.1) (P450-J) (ETHANOL INDUCIBLE) CYP2E1
102906	CYTOCHROME P450 IIF1 (EC 1.14.14.1) CYP2F1.
M14565	CYTOCHROME P450 XIA1, MITOCHONDRIAL PRECURSOR (EC 1.14.15.6) (P450(SCC)) (CHOLESTEROL SIDE-CHAIN CLEAVAGE ENZYME) (CHOLESTEROL DESMOLASE) (CYP11A1.
X55764	CYTOCHROME P450 XIB1 PRECURSOR (P450C11) (STEROID 11-BETA-HYDROXYLASE) (EC 1.14.15.4) CYP11B1 OR S11BH.
M12792; (M23280)	M12792: (M23280) CYTOCHROME P450 XXIB (EC 1.14.99.10) (STEROID 21-HYDROXYLASE) (P45J-C21B) CYP21B OR CYP21 OR CYP21A2.
107765	LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE)
J05459	CESZ. GLUIATHIONE S-TRANSFERASE MU 3 (EC 2.5.1.18) (GSTM3-3) (CLASS-MU) GSTM3 OR GST5.
D13889	GLUTATHIONE REDUCTASE
X15722	GLUTATHIONE S-TRANSFERASE MICROSOMAL CLUTATHIONE S-TRANSFERASE MU 1)
303/40 X08020	
X15480	GLUTATHIONE S-TRANSFERASE A1-1 (Glutathione S-transferase (GST) Ha subunit 1)
M14777	GLUIAIHIONE PERONIDASE CHITATHIONE CIDANISEPDASE (THETA 1)
MZ1304 AF010316	GLUTATHIONE-S-TRANSFERASE HOMOLOG
105779	SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRAIASE) (CYLOSOLIC FPOXIDE HYDROLASE) (CYLOSOLIC)

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
M57899	UDP-GLUCURONOSYLIRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1A) (UGT1-1) (UGT1-01) (UGT1.1) (UGT1A1) (BILIRUBIN SPECIFIC ISOZYME 1) (UGT1A) (HUG-BR1) UGT1 OR GNT1.
S55985	UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1B) (UGT1*2) (UGT1-02) (UGT1.2) (UGT1A2) (UGT1B) (HLUGP4) UGT1 OR GNT1.
M84127	UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1C) (UGT1*3) (UGT1.3) (UGT1.3) (UGT1A3) (UGT1A3) (UGT1C) UGT1 OR GNT1.
M57951	UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPG1) (UGT-1D) (UGT1*4) (UGT1-04) (UGT1.4) (UGT1A4) (UGT1D) (BILIRUBIN SPECIFIC ISOZYME 2) (HUG-BR2) UGT1 OR GNT1.
104093	UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT-1F) (UGT1*6) (UGT1-06) (UGT1.6) (UGT1A6) (UGT1F) (PHENOL SPECIFIC) UGT1 OR GNT1.
X71480	CYTOCHROME P450 IVA11 (EC 1.14.14.1) (FRAGMENT) CYP4A-11.
X83573	ARYLSULFATASE E PRECURSOR (EC 3.1.6) (ASE) ARSE.
X92106	BLEOMYCIN HYDROLASE (EC 3.4.22) (BLM HYDROLASE).
M65212	CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) (CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)) COMT.
228409	COPROPORPHYRINOGEN III OXIDASE PRECURSOR (EC 1.3.3.3) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) (COX) CPO.
V09501	NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R) DIA1.
U12778	ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) ACADSB.
M74542	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (CLASS 3) ALDH3.

GenBank #	STRESS RESPONSE REGULATORS AND EFFECTORS
X53463	GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE-RELATED PROTEIN 2) (GPRP) GPX2.
X71973	PHOSPHOLIPID HYDROPEROXIDE GLUTHATIONE PEROXIDASE (EC 1.11.1.9) (PHGPX) GPX4.
M63012	SERUM PARAOXONASE/ARYLESTERASE 1 (EC 3.1.1.2) (EC 3.1.8.1) (PON 1) (SERUM ARYLDIAKYLPHOSPHATASE 1) (A-ESTERASE 1) (AROMATIC ESTERASE 1) PON1 OR PON.
148513	SERUM PARAOXONASE/ARYLESTERASE 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (SERUM ARYLDIAKYLPHOSPHATASE 2) (A-ESTERASE 2) (AROMATIC ESTERASE 2) PON2.
L48516	SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) (FRAGMENT) PON3.
862904	THIOPURINE S-METHYLTRANSFERASE (EC 2.1.1.67) (THIOPURINE METHYLTRANSFERASE) TPMT.
102932	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) PPARA OR PPAR
107592	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA) (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1) PPARB OR PPARD.
	HOUSEKEEPING GENES
M26880	UBIQUITIN
M86400	PHOSPHOLIPASE A2 LIVEOVANTHINE-CITANINE PHOSPHORIBOSYLTRANSFERASE
X01677	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
K00558	TUBULIN ALPHA
M11886	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN
(MHC)	90Z BETA-ACTIN
X56932	23 kD HIGHLY BASIC PROTEIN
U14971	RIBOSOMAL PROTEIN S9
	NICO ATIVE CONTROLS
	NEGALIVE CONTROLS

Oncogene and Tumor Suppressor Gene Array

5

In the oncogene and tumor suppressor gene array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with cellular proliferative diseases, specifically neoplastic diseases. Genes of interest that may be represented on the array include: oncogenes and tumor suppressor genes. In a specific oncogene and tumor suppressor gene array of interest, the spots are as provided in Table 6.

TABLE 6

# 4 = 0	Cone Name
V00568	MYC PROTO-ONCOGENE PROTEIN
M29366	HER3 (ERB-B3)[Epidermal growth factor receptor (avian enythroblastic leukernia viral (v-erb-
NADARA A	b) oncogene homolog)]
X03663	MACROPHAGE COLONY STIMULATING FACTOR RECEPTOR [c-fms proto-oncogene]
Z12020; [M92424]	24 MDM2 PROTEIN (P33-A330CIATED PROTEIN) + MDM2-A (GE. G3313) + MDM2 PROTEIN) + MDM2-A (GE. G3313)
X02811; [X027	X02811; [X02744; PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
M12783]	(PDGF-2) (BACAPLERMIN) (C-SIS)
X01394	TUMOR NECROSIS FACTOR [TNFa]
K03222	TRANSFORMING GROWTH FACTOR-ALPHA
X02812	TRANSFORMING GROWTH FACTOR BETA [1]
M15024	MYB PROTO-ONCOGENE PROTEIN
M14694	CELLULAR TUMOR ANTIGEN P53
M19154	TRANSFORMING GROWTH FACTOR BETA [2]
X06182	C-kit
L07594	TGF-BETA RECEPTOR TYPE III
X07282	RETINOIC ACID RECEPTOR BETA-2
X13293	MYB-RELATED PROTEIN B [8-myb]
M24898	V-ERBA RELATED PROTEIN EAR-1 [Thyroid hormone triiodothyronine receptor c-erbA,ear-
K03193; [X00588; X00663; U48722]	i88; EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112). (EGFR) 22] (ERBB1)
X12794	V-ERBA RELATED PROTEIN EAR-2
X12795	COUP TRANSCRIPTION FACTOR [V-erbA related ear-3 protein]
U11732	ETS-RELATED PROTEIN TEL
U18422	DP2 (Humdp2), dimerization partner of E2F
L07868	ERBB4 [EPIDERMAL GROWTH FACTOR RECEPTOR]
J04111	袬
M33294	TUMOR NECROSIS FACTOR RECEPTOR [Tumor necrosis factor receptor 1 (55kD)]
M11730	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE

1 12260	
L12261	HEREGULIN ALPHA [Recombinant glial growth factor]
M27288	ONCOSTATIN M
M59964	STEM CELL FACTOR (C-KIT LIGAND)
M76125	AXL (TYROSINE-PROTEIN KINASE RECEPTOR UFO)
X06182	C-KIT PROTO-ONCOGENE [mast/stem cell growth factor receptor]
X06374	PLATELET-DERIVED GROWTH FACTOR A CHAIN
D13866	ALPHA-CATENIN
D17517	SKY (DTK) (TYRO3) (RSE)
L11353; Z22664;	2664; MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like protein)(neurolibromatosis 2)
X72657; L27133	
L13738	
L14837	
L16785	NUCLEOSIDE DIPHOSPHATE KINASE B [c-myc transcription lactor (pur)]
L19067	TRANSCRIPTION FACTOR P65
L20422	PROTEIN ETA [14-3-3 PROTEIN ETA]
L22075	≅
L25259	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 [CD28 antigen ligand 2, B7-2 antigen]
L33264	CDC2-RELATED KINASE PISSLRE
M13150	MAS PROTO-ONCOGENE
M31213; [M31213; [M57464] PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR (EC
	2.7.1.112) (C-RET) [Papillary thyroid carcinoma-encoded protein]
M31899	DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS [DNA-REPAIR TELICASC (ETTOCK)
M32865	ATP-DEPENDENT DNA HELICASE II (70 KD SUBUNIT) [Thyroid autoantigen 70kD (Ku
	antigen)]
M34960	TRANSCRIPTION FACTOR IID
M36089	DNA-REPAIR PROTEIN XRCC1
M54915	PIM-1 PROTO-ONCOGENE (SERINE/THREONINE-PROTEIN KINASE)
M60915	NEUROFIBROMIN [neurofibromatosis protein type I (NF1)]
700001	COLOBECTAL MUTANT CANCER PROTEIN

	GenBank #	ā
	M62810	MtTF1 [TRANSCRIPTION FACTOR 1 MITOCHONDRIAL]
	M81750	MYELOID CELL NUCLEAR DIFFERENTIATION ANTIGEN
	M81840	TRANSFORMING PROTEIN MAF [NRL gene product]
	M83234	Y BOX BINDING PROTEIN-1 [Nuclease-sensitive element DNA-binding protein]
	U02082	GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM1
	U03056	HYALURONIDASE [turnor suppressor (LUCA-1)]
	U07236	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK [Lymphocyte-specific protein
		tyrosine kinase
	U09579; [L25610]	CYCLIN-DEPENDEN I KINASE INHIBITOR 1 (MELANOMA DIPFERENTIATION ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1)
		(WAF1) (CDKN1A) (CDKN1) (SD11) (PIC1) (CAP20)
	X07024	TRANSCRIPTION INITIATION FACTOR TFIID (250 KD SUBUNIT) [CG1 protein inv. in cell protein inv. in cell
	X15218	SKI ONCOGENE
	X15219	SKI-RELATED ONCOGENE SNON
- Annual Contract of the Contr	X51630	WILMS TUMOR PROTEIN
	M81933	cdc25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48)
	M92287	CYCLIN D3
	S85655	PROHIBITIN
	X03484	RAF PROTO-ONCOGENE (SERINE/THREONINE-PROTEIN KINASE)
	X16416	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL
	X59798; [M64349]	CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE)
	D13639 [M90813]	CYCLIN D2
	HT2291; [K03214;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC) (C-
	X03996]	SRC).
	X75042	C-REL PROTO-ONCOGENE PROTEIN
		- 1
	L25080	-
	X75342	SHB ADAPTOR PROTEIN [A Src HOMOLOGY 2 PROTEIN]
	L26584	CDC25 [GUANINE NUCLEOTIDE RELEASING PROTEIN]
	X76132	TUMOR SUPPRESSOR PROTEIN DCC

		A. A
	GenBank #	Gene Name
	L27211	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)
		(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). (CDKN2A)
	M13228	N-MYC PROTO-ONCOGENE PROTEIN
\ <u>\</u>	M15400	RETINOBLASTOMA-ASSOCIATED PROTEIN [retinoblastoma susceptibility]
2	M15990	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES
	M19720	L-MYG-2 PROTEIN
4	M19722	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR) (C-
		FGR).
	M73812	CYCLIN E (G1/S-SPECIFIC)
	M74088	ADENOMATOUS POLYPOSIS COLI PROTEIN
	U25994	TYROSINE-PROTEIN KINASE LYN [cell death protein RIP]
	U40343; [U20498]	CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
	U43746	BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN
	X02751	TRANSFORMING PROTEIN P21 [N-ras]
	X16706	FRA-2 [fos-related antigen 2]
	X16707	FRA-1 [fos-related antigen 1]
	X51521	EZRIN [Villin 2]
	X56681	TRANSCRIPTION FACTOR JUN-D
	X59932	TYROSINE-PROTEIN KINASE CSK [C-SRC-kinase]
	X86779	FAST KINASE
	X87838	BETA-CATENIN
	Z29090	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT ALPHA ISOFORM
	M14745	BCL2
	D38305	108
	L16464	ETS-RELATED PROTEIN PE-1 [ETS oncogene (PEP1)]
	L29216	PROTEIN KINASE CLK (CLK2)
	L29220	PROTEIN KINASE CLK (CLK3)
	L29222	PROTEIN KINASE CLK (CLK1)
	U10564	CDK TYROSINE 15-KINASE WEE1Hu

	Land John A
Genbank #	Gelle Nallie
U22398	CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR 1C)
	r3/) (r3/nir2)
U24166	EB.
U26710	PROTO-ONCOGENE C-CBL
U33841	ATAXIA TELANGIECTASIA (ATM)
U35735	RACH1
U40282	INTEGRIN-LINKED KINASE (ILK) [MIXED LINEAGE KINASE 2]
U41816	C-1
U43408	FOCAL ADHESION KINASE [tyrosine kinase (Tnk1)]
U57456	MOTHERS AGAINST DPP PROTEIN [chromosome 4 Mad homolog Smad1; transforming
	growth factor-beta signaling protein-1 (bsp-1)]
008090	semaphorin (CD100)
U61262	TUMOR SUPPRESSOR PROTEIN DCC [neogenin]
U63139	DNA REPAIR PROTEIN RAD50
M81934; [S78187]	cdc25B; M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). (CDC25Hu2)
U17075; [L36844]	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE
	TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B).
U84119	LACTOFERRIN (DELTA)
X74262	RBA/p48
X85133	RBQ1 retinoplastoma binding protein
Z29083	5T4 ONCOFETAL ANTIGEN
L23959	E2F-related transcription factor (DP-1)
L25676	SERINE/THREONINE PROTEIN KINASE PITALRE
L26081	semaphorin III
L37882	frizzled
L20861	Wnt-5a
M29039	jun B TRANSACTIVATOR
M34065	cdc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).
M73980	Notch1
M95712	raf,b-
M99437	notch group protein (N)
U15642	E2F-5
U33920	semaphorin V

	# 7ac0ac	Gene Name
	Gelibalin #	יומוים
	U43318	nizzed 5
	U46461	dishevelled homolog (DVL)
	U49262; [U75651]	dishevelled (DVL) + dishevelled 3 (DVL3)
:	L34075	FKBP-RAPAMYSIN ASSOCIATED PROTEIN (FHAP)
	X07876	WNT2 OR IRP
	1 40027	glycogen synthase kinase 3
	X66360	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2
	X66362	SERINE/THREONINE PROTEIN KINASE PCTAIRE-3
	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1
	X74594	RB2/p130
	X85134	RBQ-3
	271621	Wnt-13
	AB000220	semaphorin E
	AF001954	growth inhibitor p33ING1 (ING1)
	AF007111	MDM2-like p53-binding protein (MDMX)
	D89667	C-myc binding protein
	U29343	HYALURONAN RECEPTOR (RHAMM)
	U66469	p53-dependent cell growth regulator CGR19
	U76638	BRCA1-ASSOCIATED RING DOMAIN PROTEIN
	U82169	frizzled homolog (FZD3)
	U84401	smoothened
	U90875	cytotoxic ligand TRAIL receptor
	U95299	Notch4
	Y11416	p73, a monoallelically expressed p53-related protein
	X91940	WNT-8B
	X97057	WNT-10B
	Y10479	E2F-3
	Y11306	beta catenin/TCF-4
	U38276	SEMAPHORIN-1
	U77493	Notch2
	K00650	C-los
	X53795	CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN R2) (C33 ANTIGEN) (IA4) (METASTASIS SUPPRESSOR KANGAI 1) (SUPPRESSOR OF TUMORIGENICITY-6).
	1 38518	Sonic hedgehog (SHH)
:	10001	K-BAS ONCOGENE
	M54900	

	# August	Space Name
	Meate7	Akt1 (rac protein kinase aloha, protein kinase B, c-Akt)
	MOSTO.	DEDAGETINORI ASTOMA-RINDING PROTEIN)
	Ī	חסב ו(טבווואסריים מוומים של היים)
	U23435; U31089	Abl interactor 2 (Abi-2) + Abl binding protein 3 (AbiBP3) [ArgBP1B]
	M96577	E2F-1 pRB-binding protein
	U24163; [U91903;	U24163; [U91903; frizzled-related FrzB (Fritz) (frezzled (fre))
	U68057]	
	L05148	TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KD ZETA-ASSOCIALED
		PROTEIN) (ZAP70)
	M97935	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCHIPTION 1-ALPHA/BETA TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) (STAT1)
	1110087 X58957	TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE
		KINASE)(AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR
		KINASE) (BPK) (BIK) (AGMX1)
	AF016268	death receptor 5 (DR5)
	M35296	TYROSINE-PROTEIN KINASE ABL2 (EC 2.7.1.112) (TYROSINE KINASE ARG) (ABLL)
	U18671 M97934	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2 (P113) (STAT2)
	U47686	SIGNAL TRANSDUCER AND TRANSCRIPTION ACTIVATOR 5B (STAT5B)
	M80629	CDC2-RELATED PROTEIN KINASE CHED
	S66431	RBP2 retinoblastoma binding protein
	U04045; [L47583]	DNA MISMATCH REPAIR PROTEIN MSH2
	U29656	DR-NM23
	U43148	patched homolog (PTC)
	J02958	MET
	U49089	neuroendocrine-dig (NE-dig) a novel human homolog of the Drosophila discs large (dig) tumor suppressor protein interacting with the APC protein
	U54777	DNA MISMATCH REPAIR PROTEIN MSH6 (mutS - ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160)
	01000	SEDINE/THREONING. PROTEIN KINASE KKIAI RE
···	Xee358	

Cell-Cell Interaction Array

5

In the cell-cell interaction array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with cell-cell interaction, e.g. cell-cell signaling. In a specific cell-cell interaction array of interest, the spots are as provided in Table 7.

TABLE 7

\$ 7000 C	CELL INTERACTION (Gene Names)
delibalin #	THE MECHANICAL PROPERTY IN THE PROPERTY OF THE
M32315	
X01394	IOH (INFa)
D12614	LYMPHOTOXIN-ALPHA [formerly tumor necrosis factor beta (INF-beta)]
M12807	T-CELL SURFACE GLYCOPROTEIN CD4
M14648	VITRONECTIN RECEPTOR ALPHA [Integrin, alpha V; antigen CD51]
X75208	TYROSINE-PROTEIN KINASE RECEPTOR EPH-3
X74764	TYROSINE-PROTEIN KINASE CAK [Tyrosine kinase, receptor K1]
M18391	TYROSINE-PROTEIN KINASE RECEPTOR EPH
U08839 [M83246;	46; UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED
X51675]	FORM PRECURSOR (U-PAR) (MONOCYTE ACTIVATION ANTIGEN MO3) (CD8/
	ANTIGEN)
M33294	TUMOR NECROSIS FACTOR RECEPTOR [Tumor necrosis factor receptor 1 (35kD)]
Y00285	CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR Insuline-like growin
	factor receptor II, IGFR-2]
L07414	CD40
L08096;	CD27 (CD70 ANTIGEN)
[Se6333]	
L09753	CD30
M35410	اب
M63928	_
M67454	FASL RECEPTOR [Fas antigen, APO-1 antigen]
M83554	CD30L RECEPTOR [Lymphocyte activation antigen CD30; Ki-1 antigen]
X60592	CD40L RECEPTOR [Cdw40 nerve growth factor receptor-related B-lymphocyte activation
	molecule
D13866 [D14705	705 ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN) (ALPHA E-CATENIN)
L23805; L22080	[08]
D25303;	integrin alpha9
[L24158]	
J03132	INTERCELLULAR ADHESION MOLECULE-1
J04536	LEUKOSIALIN (sialophorin (CD43))
L11353; Z22664;	564; MERLIN (SCHWANNOMIN) (moesin-ezrin-radixin-like protein)(neurofibromatosis 2)
X72657; L27133	133
L13616	Focal adhesion kinase
L14837	TIGHT JUNCTION PROTEIN 20-1
L16785;	NUCLEOSIDE DIPHOSPHATE KINASE B (EC 2.7.4.6) (NDF B) (NDP KINASE B) (NM23-112)
[M36981]	(C-MYC PURINE-BINDING TRANSCHIPTION TACTOR FOLD.

GenBank#	CELL INTERACTION (Gene Names)
1 20815	
1.25259	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 [CD28 antigen ligand 2, B7-2 antigen]
L34774	opioid binding cell adhesion molecule
M15476	UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOH (EC 3.4.21.73) (UPA) (UPA
M15518; [TISSUE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (T-PA) (T-
X07393; M18182]	X07393; M18182] PLASMINOGEN ACTIVATOR).
M18082:[PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-
J026851	SERPIN) (UROKINASE INHIBITOR).
M21097	CD19 B-LYMPHOCYTE ANTIGEN [Differentiation antigen (CD19)]
M23197	CD33 MYELOID CELL SURFACE AN I IGEN Differentiation antigen (CD33)
M28882	~
M30257	VASCULAR CELL ADHESION PHOTEIN (Vascular cell adriesion molecule 1)
M30640	E-SELECTIN (Endothelial leucocyte adnesion molecule i (ELAMILI)
M34064 [X57548;	M34064 [X57548; CADHERIN-2 (N-CADHERIN)
X54315; S42303]	
M54992	z
M59040	CD44 ANTIGEN HEMATOPOIETIC FORM [Cell adhesion molecule (CD44)]
M63618	bullous pemphigoid antigen
M74387	L1CAM
M74777	
U01160	
U03056	8
U07819	CONTACTIN [Contactin 1 (CN1N1)]
U15979	DELTA-LIKE PROTEIN [dlk]
X16841	N-CAM (NEURAL CELL ADHESION MOLECULE, PHOSPHATID TLINOSITOL-LINAED
	ISOFORM; CD56]
X70326	1
X74979	TYROSINE-PROTEIN KINASE CAK [EDDR1; IHK E]
Z26317 [S64273]	desmoglein 2
L25080	TRANSFORMING PROTEIN RHOA [proto-oncogene mod, munitum resistance protein]
X76132	DCC
102703	PLATELE! MEMBHANE GLYCOPHOTEIN IIIA

# 14 C	CELL INTERACTION (Gene Names)
.104145	INTEGRIN ALPHA M [Neutrophil adherence receptor alpha-M subunit; Complement
	component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha
	polypeptide]
105633	integrin beta5
L12002;	integrin alpha4
[X16983]	
125851	integrin alphaE
L36531	integrin alpha8
M15395	LEUKOCYTE ADHESION PROTEIN (CELL SURFACE ADHESION GLYCOPROTEINS LFA-
	1, CR3 AND P150,95, BETA-SUBUNIT
M28249;	integrin alpha2 [very late antigen-2 (vla-2)/collagen receptor alpha-2 subunit]
[X17033]	· Index Contributed
M34480	INTEGRIN ALPHA 2B [PLATELET MEMBRANE GLYCOPHO I EIN IIB (GPIID); antigen
	CD41B]
M35198	integrin beta6
M59911	integrin alpha3
M62880	integrin beta7
M73780	integrin beta8
M81695	INTEGRIN ALPHA X (LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN;
	antigen CD11C (p150)]
X06256	E
97979X	FIBRONECTIN RECEPTOR (BETA SUBUNIT) (INTEGRIN BELA 1)
X53586;	integrin alpha6
[X59512]	
X53587;	integrin beta4
[X52186]	
X68742	integrin alpha
X74295	integrin alpha7B
Y00796	INTEGRIN ALPHA L (LEUKOCYTE ADHESION GLYCOPROTEIN LFA-1 ALPHA CHAIN;
	antigen CD11A (p180)]
D38122	FAS ANTIGEN LIGAND
M74088;	APC (DP2.5)
[M73548]	(7)14 (1)
U43522;	Protein tyrosine kinase Pyk2 (Cell adhesion kinase-beta, CAK-beta) (FAK2)
X51521	Ezrin (cytovillin 2)
130100	

TABLE 7 (CONT)

# Juco	CELL INTERACTION (Gene Names)
X87838 [719054	Vazasa 17190541 BETA-CATENIN
L11015	-BETA
U57059	FAS ANTIGEN LIGAND [TNF-related apoptosis inducing ligand TRAIL; Apo-2 ligand]
D45132	ANNEXIN [zinc finger protein RIZ]
M68516;	PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI) (PROTEIN C INHIBITOR)
[102639]	(PLASMINOGEN ACTIVATOR INHIBITOR-3) (PAI3).
U40282	
U43408	FOCAL ADHESION KINASE [tyrosine kinase (Tnk1)]
008090	
U61262	TUMOR SUPPRESSOR PROTEIN DCC [neogenin]
L11370	protocadherin 42
X78817	RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAAU131).
X85978	TAX1, AXONIN-1/TAQ1
L11373	protocadherin 43
X89576	MMP-17 (MT4-MMP)
Y00815	LAR
Z30183	TIMP-3 (mitogen-inducible gene 5, mig-5)
Z35227	ras-like small GTPase TTF
D26512,	MMP-14 (MT1-MMP)
[X83535]	
D31784	CADHERIN-6
D50477	MMP-16 (MT3-MMP)
D83542	CADHERIN-14 MUSCLE-CADHERIN PRECURSOR (M-CADHERIN) (CADHERIN-14)
J03210, [J0547	J03210, [J05471] MMP-2 (gelatinase A)
J05070, [D100	J05070, [D10051] MMP-9 (gelatinase B)
J05556	MMP-8 (collagenase-2)
L20688	rho GDP-dissociation inhibitor protein 2 (Ly-GDI)
L26081	semaphorin III
L34056	CADHERIN-11 (OSTEOBLAST-CADHERIN) (OB-CADHERIN)
L34057; [L334]	L34057; [L33477] CADHERIN-12 (BR-CADHERIN) (N-CADHERIN 2) (CADHERIN, NEURAL 17PE, 2)
_	

TABLE 7 (CONT)

	7	CELL INTEDACTION (Cana Names)
5	Gendalik #	OCELL IN ELICATION TO THE PROPERTY OF THE PROPERTY OF CANHERIN
<u> </u>	L34058;	CADHEKIN-13 I-CADHERIN PRECONSON (INGINORIED-CADIEI IIIV) (III-CADHERIIV)
<u>2</u>	[U59289;	(HEART-CADHERIN)
Ď	U59288]	TOTAL CONTRACTOR OF THE PROPERTY OF THE PROPER
3	L34059	CADHERIN-4 RETINAL-CADHERIN PRECURSOR (H-CADHERIN) (H-CAD)
<u> </u>	L34060	CADHERIN-8
2	M23410	PLAKOGLOBIN (DESMOPLAKIN III)
Σ	M94151	ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-2)
Š	U24152	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1) (P65-PAK) (P21-
		ACTIVATED KINASE) (ALPHA-PAK)
Ö	U24153	p21-activated protein kinase (Pak2)
n	U33920	semaphorin V
בו	U43318	frizzled 5
×	X04429	PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR, ENDOTHELIAL (PAI-1)
×	X13916	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PHOTEIN 1 PRECURSOR (LRP)
>	4 4707	TUDOWADORDONIN 1 PRECIPSOR
× .	A14/8/	I II TOWNED ON DEATH I I I I I I I I I I I I I I I I I I I
	L40027	glycogen synthase surface of
×	X54412	collagen type IX alpha-1
×	X56654	desmoglein type 1
×	X56807	DSC2 mRNA for desmocollins type 2a and 2b
×	X61587	rhoG
×	X63629	CADHERIN-3 PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN)
×	X69550	rho GDP-dissociation Inhibitor 1
×	X75308	MMP-13 (collagenase-3)
×	78565	TENASCIN-C
×	X79981;	CADHERIN-5 VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (/84
<u> </u>	[X59796]	ANTIGEN) (CD144 ANTIGEN).
2	M11313	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M)
×	X95282	Rho8 protein
×	X95456	Rho7 protein
<u></u>	Y07923	Rho6 protein
2	Z13009	CADHERIN-1(E-CADHERIN) (UVOMORULIN) (CAM 120/80)
7	Z15009	laminin
7	Z48482	MMP-15 (MT2-MMP)
7	AB000220	semaphorin E
	AF003522	Delta

TABLE 7 (CONT)

GenBank #	CELL INTERACTION (Gene Names)
705845	rhoHP1
D03013	Zvxin related protein ZRP-1
AL0003/4	HYAI LIBONAN RECEPTOR (RHAMM)
M24795	PLATELET GLYCOPROTEIN IV (GPIV) (GPIIIB) (CD36 ANTIGEN) (PAS-4
20177111	PROTEIN)
U72661	NINJURIN-1
U76456	TIMP-4
U82532	GDI-dissociation inhibitor RhoGDIgammma
X92521	MMP-19
Y07604	nm23-H4; NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.9) (NOCLEOSIDE 3 DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK).
V11306	beta catenin/TCF-4
U38276	SEMAPHORIN-1
U94354	lunatic fringe
U02570	CDC42 GTPase-activating protein
X05199	PLASMINOGEN PRECURSOH (EC 3.4.21.7)
X05231	MMP-1 (collagenase-1)
X53795	CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN PS) (233 ANTIGEN (177.9).
	(METASIASIS SOFT ITEROOF IN THE TABLE SOFT ITEROOF ITE
L38517	indian hedgehog protein (ITIT)
M31470	ras-like protein TC10
M34189	integrin beta1
X83929;	desmocollin type 3 + desmocollin type 4
[D17427]	
L23808	MMP-12 (metalloelastase)
125081	rhoC (H9); SMALL GIPase (rhoC)
M29870;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTITATE 1 (12111701) (1310 - 13
[M31467]	TC25)
M64595;	RAS-RELATED C3 BOTULINUM LOXIN SUBSTINATE ((721-11002)
[M29871]	
X05232	MMP-3 (stromelysin-1)
X06820	rhoB
X07820,	MMP-10 (stromelysin-2)
[M30461]	documenting type 1
X72925	

GenBank #	CELL INTERACTION (Gene Names)
X94991;	Zyxin + Zyxin-2
[X95735]	
U52111	PLEXIN
M38690	CD9
M54995; M3844	M54995; M38441 PLATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE
	BETA-THROMBOGLOBULIN (BETA-TG), NEUTROPHIL-ACTIVATING PEPTIDE 2 (NAP-2))
1 20471	extracellular matrix metalloproteinase inducer EMMPRIN
M57730 M37476	+
	(LERK-1) (IMMEDIALE EARLY RESPONSE PROTEIN BOT) (TOMON NECROSISTEM FOR STATEM BOT)
1107695	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
	KINASE RECEPTOR HTK).
U09304	EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2)
	(LERK-2) (ELK LIGAND PRECURSOR) (ELK-L).
U41766	metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9)
U26403	EPHRIN-A5 PRECURSOR (EPH-RELATED RECEPTOR LYROSINE KINASE LIGAND /)
	(LERK-7) (AL-1).
AF035752	caveolin-2
U32114	10 CINA CLI TOCHUM TIMOCOME TOTAL
U66406	EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR 1 YROSINE KINASE LIGAND 8)
	(LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBHANE LIGAND ELK-L3).
X95425	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
	KINASE RECEPTOR ERK-1) (EPH HOMOLOGI MINASE-1) (NECEPTORI MOTEUR)
718951 S49856	
L38734	
	(LERK-5) (HTK LIGAND) (HTK-L).
L40636	EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
	KINASE RECEPTOR EPH-2) (NET).
L41939	EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (1 YHOSINE-PROTEIN EPH-
	3) (DRT)
M16591	TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P39-HCK AND P00-HCK) (HEMOPOIETIC CELL KINASE).

GenBank #	CELL INTERACTION (Gene Names)
 M59371 M36395	EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC. 27.1.112) (17HOSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE).
M63959	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MBAP) (I OW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED
	PROTEIN 1) (RAP)
M77830	desmoplakin I
M86826	IGF BINDING PROTEIN ACID-LABILE SUBUNIT
M99487	PROSTATE-SPECIFIC MEMBRANE ANTIGEN (PSM)
U04441	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN)
	(GLYCOPROTEIN 330) (FRAGMENT)
U11690	PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR(RHO/RAC GEF)
	(FACIOGENITAL DYSPLASIA PROTEIN)
U14588	Paxillin
U16296	T-lymphoma invasion and metastasis inducing TIAM1
U29656	DR-NM23
U32907	P37NB
U35113	METASTASIS-ASSOCIATED MTA1
U37139	beta 3-endonexin
U43195	Rho-associated, colled-coil containing protein kinase p160ROCK
U43527	malignant melanoma metastasis-suppressor (KiSS-1) gene
U49089	neuroendocrine-dlg (NE-dlg) a novel human homolog of the Drosophila discs large (dlg) tumor
 	suppressor protein interacting with the APC protein
U53786	envoplakin (EVPL)
U59752	cytohesin-1; Sec7p-like protein
X03124	TIMP-1 (erythroid potentiating activity, EPA)
X07819	MMP-7 (matrilysin)
X17620	NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (NDP KINASE A) (TUMOR
	METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR
	NM23) (NM23-H1).
J05593	TIMP-2 (MI)
X57766	MMP-11 (stromelysin-3)

Cytokine and Cytokine Receptor Array

5

In the cytokine and cytokine receptor array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that express cytokines or cytokine receptors. In a specific cytokine and cytokine receptor array of interest, the spots are as provided in Table 8.

TABLE 8

GenBank #	Gene Name
	INTEDICTION 2 BECEDTOR AI PHA CHAIN
MZ9696	l
X01992	INTERFERON GAMMA
J04156	
X01057	INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
A14844	INTERLEUKIN-2
M29366	PROTEIN-TYROSINE KINASE RECEPTOR ERBB-3 [Epidermal growth factor receptor (avian
	erythrobiastic leukemia viral (V-erb-b) oncogene fromology)
X04434	쒸
M29645	
X03663	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR (c-ims proto-oricogene)
M32315;	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
[M55994]	BINDING PROTEIN 2) (18PII) (P8U) (1NP-R2) (P73) (CD120B) (1NP-R2)
X02811;	PLATELET-DERIVED GROWIN PACION, B CHAIN PRECONSON (1 DOI D'OLTIN)
[X02744;	(PDGF-2) (BACAPLEHMIN) (C-SIS)
X02851	INTERLEUKIN-1 ALPHA
K02770	INTERI EUKIN IL-18ETA
M14743	INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
[M17115]	FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
•	(MAST-CELL GROWTH FACTOR) (MCGF) (IL3).
M13982	INTERLEUKIN-4
X04602;	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
[M14584]	(INTERFERON BETA-2) (HYBRIDOMA GROWIH FACTOR).
X01394	TOR [IN-a]
D12614	LYMPHOTOXIN-ALPHA [formerly tumor necrosis factor beta (TNT-beta)]
M20566	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN
X04688;	INTERLEUKIN IL-5 (B CELL DIFFERENTIATION FACTOR I) (I-CELL REFLACING
[J03478]	FACTOR) (EOSINOPHIL DIFFERENTIATION FACTOR)
M28622	INTERFERON BE IA
M11220	IMULATING PACTOR
K03222	TRANSFORMING GROWTH FACTOR-ALPHA
100209;	LEUKOCYTE INTERFERON ALPHA
[100207]	
X02812	
X03438	GRANULOCYTE COLONY-S IMULA IING FACTON [G-CSF]
M19154	4
X04571	H FACTOR KIDNEY [EGF]
J03171	Hulen. ALPHA -REC (INTERFERON ALPHA-BETA RECEPTION ALPHA CHAIN)
M57627	INTERLEUKIN-10
M26062	INTERLEUKIN-2 RECEPTOR BE IA CHAIN

	1
GenBank #	ļ
M74782	-
X52425	- 1
M75914	
X77722	ا≥
X72755	GAMMA INTERFERON INDUCED MONOKINE [Humig]
D11086	CYTOKINE RECEPTOR COMMON GAMMA CHAIN [Interleukin 2 receptor gamma chain]
M20132	ANDROGEN RECEPTOR
M73238	Œ
J03143	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN
M60459	ERYTHROPROTEIN RECEPTOR
L00587	~
M62424	THROMBIN RECEPTOR (Coagulation factor II (thrombin) receptor)
107594	TRANSFORMING GROWTH FACTOR-BETA LYPE III HECEPTOR
M84747	INTERLEUKIN-9 RECEPTOR
U00672	INTERLEUKIN-10 RECEPTOR
M14764	LOW-AFFINITY NERVE GROW II FACION RECEPTION (CC 2 7 1 113)
X60957	TYROSINE-PROTEIN KINASE RECEPTOR TE-T PRECONSON (EC. 2.7.1.1.1.2.).
[283/16]	CONTRACT AND TAILURING COOMITHE EACTOR RECEPTOR 3 PRECIIRSOR (EC
X68203;	VASCULAH ENDU INELIAL GROWIIII ACI CILILIZCEI TOTTOTTETOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTO
11423423	
043143	NI HOOMOGINE
M16552	I THOMBOMODULIN MICHAEL DECEDIOR TYPE-14
M87290	ANGIOLENSINE HECEFION FITE TO THE TOTAL TO
M83941	TYROSINE-PROTEIN KINASE MECEPTION EIN I
M76673	FMLP-RELATED RECEPTOR I
M97675	TRANSMEMBRANE RECEPTOR HOH1
L04947;	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC
[X61656]	L.
M91196	INTERFERON CONSENSUS SEQUENCE BILLION FINA FINAL DIVINE PROFESSION FOR THE PROFESSION FOR
X75208	TYROSINE-PROTEIN KINASE RECEPTOR EPH-3
U05012	- 1
X74764	TYROSINE-PROTEIN KINASE CAK [Tyrosine kinase, receptor 1K1]
K03193;	EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112). (EGFH)
(X00588;	(ERBB1)
X00663;	
[048722] [040003	DI ATELET ACTIVATING FACTOR RECEPTOR
010202	TYROSINE-PROTEIN KINASE RECEPTOR EPH
A09781	INTERFERON-GAMMA RECEPTOR
1103101	TYROSINE KINASE RECEPTOR TRK-B
041210	

M86492 L07868 M27492 M33294 M37435 M11730 D10923		
M27495 M27495 M32295 M37435 M11736 D10929		CLIA MATHRATION FACTOR RETA
M27497 M32297 M37437 M11730 D10929		CODD A CONCENSAL CONSTITUTE BECEDING 1
M27499 M33299 M37439 M11730 D10923		HBB4 [EPIDEHMAL GROWIN FACION NECETION]
M33294 M37438 M11730 D10923		INTERLEUKIN-1 RECEPTOR TYPE I
M37438 M11730 D10923		
M11730		MACROPHAGE COLONY STIMULATING FACTOR-1 (M-CSF)
D10923		ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE
		HM74 [PROBABLE G PROTEIN-COUPLED RECEPTOR HM74]
D10924		HM89 [PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG]
D10925		HM145 [C-C CHEMOKINE RECEPTOR TYPE 1]
D14012		HEPATOCYTE GROWTH FACTOR ACTIVATOR
D16431		HEPTOMA-DERIVED GROWTH FACTOR
D30751;		BONE MORPHOGENETIC PROTEIN 4 (BMP-2B)
[M22490]		
103358		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FER
304130		MACROPHAGE INFLAMMATORY PROTEIN 1-BETA [Activation (Act-2)]
J05081		ENDOTHELIN-3
L06139		TYROSINE-PROTEIN KINASE RECEPTOR TIE-2 PRECURSOR (EC 2.7.1.112) (TYROSINE
-		PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL
L06622		ENDOTHELIN-1 RECEPTOR [EDNRA]
L06623		ENDOTHELIN B RECEPTOR (EDNRB)
L06801		INTERLEUKIN-13
L07414		CD40 LIGAND
960807		
L08187		CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA [cytokine receptor EB13]
109753		CD30
L12260;		RECOMBINANT GLIAL GROWTH FACTOR + NEU DIFFERENTIATION FACTOR +
U02326;	6;	HEREGULIN
M94165		Į
L12261		HEREGULIN ALPHA (Recombinant glial growth factor)
L15344		INTERLEUKIN IL-14
L36052		THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING
[136051;		FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT
U11025		FACTOR) (MGDF) (THPO)
M10051	51	INSULIN RECEPTOR
M21121		RANTES PROTEIN T-CELL SPECIFIC
M21574	74	PLATELET-DERIVED GROWTH FACTOR RECEPTOR ALPHA
M21616	16	PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA
M22488	38;	BONE MORPHOGENETIC PROTEIN 1 (procollagen C-proteinase) (pCP-2)
[050330	(S)	
M22489	39	BONE MORPHOGENETIC PROTEIN 2A

GenBank # Gene Name M22491 MACROPHOGENETIC PROTEIN 3 M22495 MACROPHOGENETIC PROTEIN 1 M23455 MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA M23567 NEUFIOMODULIN IN Incuronal growth protein 43 (GAP-M27588 M30704 MAPHIREGULIN IN Incuronal growth protein 43 (GAP-M30706) M31165 NISULIN-LIKE GROWTH FACTOR BINDING PROTEIN IN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN IN INSULIN-LIKE GROWTH FACTOR PRECEPTOR INSULIN-LIKE GROWTH FACTOR PRECEPTOR INSULIN-LIKE GROWTH FACTOR RECEPTOR INSULIN-LIKE GROWTH FACTOR RECEPTOR M35477 M35410 PLACENTAL RIBONUCLEASE INHIBITOR IRlabonuc M35772. M67281 PERMEABILITY FACTOR) (VPF). M673882 PLACENTAL RIBONUCLEASE INHIBITOR IRlabonuc M37722. M673883 PASIC FIBROBLAST GROWTH FACTOR RECEPTOR RIBONUC M37722. M6738893 M673889 M673894 PEIOTROPHIN PRECLIRSOR (PTN) (HEPARIN-BINI M57389. M673894 MOLECULE) (HB-GAM) (HEPARIN-BINI GROWT (M3781489) M673895 MOLECULE) (HB-GAM) (HEPARIN-BINI GROWT (M3780) M673896 INTERLEUKIN-F SECRETED PROTEIN 1-309 M67380 INTERLEUKIN-T SECRETED PROTEIN 1-309 M60718 M60718 M60718 M60718	Gene Name BONE MORPHOGENETIC PROTEIN 3 MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA [GOS19-1] MONOCYTE CHEMOTACTIC PROTEIN 1 MONOCYTE CHEMOTACTIC PROTEIN 1 NEUROMODULIN [Neuronal growth protein 43 (GAP-43)] ONCOSTATIN M AMPHIREGULIN [schwannoma-derived growth factor] INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN 15G-6 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF). IGFBP-2 [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 INSULIN-LIKE BROWTH FACTOR BINDING PROTEIN 3 INSULIN-LIKE BROW
2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	NORPHOGENETIC PROTEIN 3 PHAGE INFLAMMATORY PROTEIN 1-ALPHA [GOS19-1] PHAGE INFLAMMATORY PROTEIN 1 NYTE CHEMOTACTIC PROTEIN 1 MODULIN [Neuronal growth protein 43 (GAP-43)] TATIN M IEGULIN [schwannoma-derived growth factor] I-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 AR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 MATA RIBONUCLEASE INHIBITOR [Ribonuclease/angiogenin inhibitor RA]
2	PHAGE INFLAMMATORY PROTEIN 1-ALPHA [GOS19-1] PHAGE INFLAMMATORY PROTEIN 1 MODULIN [Neuronal growth protein 43 (GAP-43)] TATIN M REGULIN [schwannoma-derived growth factor] 1-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN 7SG-6 AR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABBLITY FACTOR) (VPF). INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 18 CORP. (REGE.A) (FC)
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	MODULIN [Neuronal growth protein 43 (GAP-43)] TATIN M REGULIN [schwannoma-derived growth factor] 1-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN 15G-6 AR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR REGULIN FACTOR) (VPF). INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 INSULIN-LIKE BROWTH FACTOR BINDING P
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	MODULIN [Neuronal growth protein 43 (GAP-43)] TATIN M REGULIN [schwannoma-derived growth factor] 1-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN 1SG-6 AR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1850R (REGE-8) (FC
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	TATIN M REGULIN [schwannoma-derived growth factor] 1-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN 1SG-6 LAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1850R (REGE. B) (FC.
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	REGULIN [schwannoma-derived growth factor] 4-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 LAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN SEGERAL (FC
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	V-LIKE GROWTH FACTOR BINDING PROTEIN 1 NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 LAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BECERTOR 1 BROWTH FACTOR 1 BROWTH PROTEIN 1
4 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 LAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR ABILITY FACTOR) (VPF). [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 ATAL RIBONUCLEASE INHIBITOR [Ribonuclease/angiogenin inhibitor RAI]
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ABILITY FACTOR) (VPF). ABILITY FACTOR) (VPF). [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 VITAL RIBONUCLEASE INHIBITOR [Ribonuclease/angiogenin inhibitor RAI]
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ABILITY FACTOR) (VPF). [INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 VITAL RIBONUCLEASE INHIBITOR [Ribonuclease/angiogenin inhibitor RAI]
2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 VTAL RIBONUCLEASE INHIBITOR (Ribonuclease/angiogenin inhibitor RAI)
2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	NTAL RIBONUCLEASE INHIBITOR (Ribonuclease/angiogenin inhibitor HAI)
;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	TODOO! ANT COOKE! TANTOO DEPOTOD & DEFINITION (BEGIND)
1]	-IBROBLASI GROWIN TACLOR RECEIVED TO CONTRACT TO CONTR
1]	2.7.1.112) (FMS-LIKE TYROSINE KINASE-2) (C-FGH) (FGFH1) (FLG) (FGFBH) (FLIZ).
1]	(HBGF-R-ALPHA-A1) (HBGF-R-ALPHA-A2) (HBGF-H-ALPHA-A3) + FGFH SECHETED
1]	M34188)
	INTERLEUKIN-6 RECEPTOR BETA CHAIN (membrane glycoprotein gp130)
	PLEIOTROPHIN PRECURSOR (PTN) (HEPARIN-BINDING GROWTH-ASSOCIATED
	MOLECULE) (HB-GAM) (HEPARIN-BINDING GROW I'H FACTOR 8) (HBGF-8)
	(OSTEOBLAST SPECIFIC FACTOR 1) (OSF-1) (HEPARIN-BINDING NEURITE
	NOWTH PROMOTING FACTOR 1) (HBNF-1).
	PHOCYTE-SECRETED PHOTEIN 1-309
	EUKIN-11 [adipogenesis inhibitory factor]
	GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR
	- 1
	IIN-BINDING EGF-LIKE GROWTH FACTOR [DIPHTHERIA TOXIN RECEPTOR]
	HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
	TOTOETHIN A):
BRAIN-DERIVED NEUROTROPHIC I GDF-1 [GROWTH/DIFFERENTIA CSA ANAPHYLATOXIN CHEMOTAC ENDOTHELIN-2 INTERLEUKIN-12 BETA CHAIN INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	FGF-7; KEHAJINOCY I E GHOW I H FACTOR PRECORSON (NGP) (FIBNOSEAS) GROWTH FACTOR-77 (HBGF-7).
GDF-1 [GROWTH/DIFFERENTIA CSA ANAPHYLATOXIN CHEMOTAC ENDOTHELIN-2 INTERLEUKIN-12 BETA CHAIN INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	-DERIVED NEUROTROPHIC FACTOR
C5A ANAPHYLATOXIN CHEMOTAC ENDOTHELIN-2 INTERLEUKIN-12 BETA CHAIN INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	[GROWTH/DIFFERENTIATION FACTOR 1]
INTERLEUKIN-12 BETA CHAIN INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	VAPHYLATOXIN CHEMOTACTIC RECEPTOR
INTERLEUKIN-12 BETA CHAIN INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	THELIN-2
INTERLEUKIN-12 ALPHA CHAIN FASL RECEPTOR [Fas antigen, A	LEUKIN-12 BETA CHAIN [Natural killer cell stimulatory factor, p40]
FASL RECEPTOR Fas antig	LEUKIN-12 ALPHA CHAIN [Natural killer cell stimulatory factor, p35]
	LEUKIN-8 RECEPTOR (ALFA, HIGH AFFINITY)
M73482 NEUROMEDIN-B RECEPTOR	OMEDIN-B RECEPTOR

8	ConBank #	Gene Name
		uebatocyte GBOWTH FACTOR-LIKE (macrophage-stimulating protein (MST1))
Σ	M/41/6	TIET ALOCALE DIOMETRIA PRINTED BECEDED HED
X X	M76125	AXL (17HOSINE-PHOLEIN NIMAGE NEOLE 1010)
Ĭ	M92381	THYMOSIN BEIA-10
Ĭ	M92934	CONNECTIVE TISSUE GROWTH FACTOR
Ĭ	M96956;	TDGF1 (TERATOCARCINOMA-DERIVED GROW I H FACTOR 1) (EPIDEHWAL GROW III)
<u>~</u>	[M96955]	FACTOR-LIKE CRIPTO PROTEIN CRITTON (CRIPTON BACTOR) (CRICTON CRICTON C
		TDGF2 (TERATOCARCINOMA-DERIVED GROWIN FACION 2) (EFIDEFINAL GIOTIN)
		FACTOR-LIKE CRIPTO PROTEIN CH3/ Control to 3 Gnow 111
Š	S59184	TYROSINE-PHOLEIN KINASE HTV INTO THE REPORT OF THE WILLIAM FOR THE CONTROL OF THE
<u>5</u>	U01134;	VASCULAR ENDOTHELIAL GHOWTH FACTOR RECEPTION TOTAL CONTOUR (CO.)
<u>×.</u>	X51602]	27.7.112) (VEGFH: I) (I THOSIME FIND I MINOSE THOSE TH
<u></u>	U02687	FL CYTOKINE RECEPTOR PRECURSON (EC 2.7.1.1.12) (TINOSINE) TOTEIN
		RECEPTOR FLISTORING CELETTIONING CONTRACTORING CONTRACTORI
Ď	U03187	INTERLEDANCE ABOUT 1 ALTON 1 A
<u>ס</u>	U03882	C-C CHEMOKINE RECEPTOR [Monocyte chemoatilacian protein receptor (mo. 1177)
		alternatively spliced
<u> </u>	U03905	מסוג איז איז איז
		allemannery spinceul
2	U04806;	SL CYTOKINE PRECURSOH (FLI 3/FLKZ LIGAND).
1	[U03858]	
2	U10117	ENDOTHELIAL-MONOCYTE ACTIVATING POLYPEP LIDE
2	U11814;	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PHECURSOR (FGFR-2) (FC 2.7.1.112)
	[M80634;	(KERATINOCYTE GROWTH FACTOR HECEPTOR) (FGFH2) (BFH-1) (NSAM-1) + N-
<u>×</u>	X52832;	SAM; K-SAM-III; K-SAM-IV
2	M35718;	
2	M87771;	
~	M8///2]	ייידרטו בוועואו זכ
	01440/	IN ENLEUKIN 13
	014/22	VACCIII DE ENDOTHEI IAI GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
	U4314Z	ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND).
	X06182	C-KIT PROTO-ONCOGENE [mast/stem cell growth factor receptor]
	X06233	[CALGRANULIN (B) [MRP-14 (calcium binding protein in macrophages,MIF-related)]
	X06234	CALGRANULIN (A) [MRP-8 (calcium binding protein in macrophages, MIF-related)]
	X06374	PLATELET-DERIVED GROWTH FACTOR (A CHAIN) [PDGF-A]
	X13967	LEUKAEMIA INHIBITORY FACTOR [cholinergic differentiation factor]
	X17543	INTERLEUKIN-9
	X17648	GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPRA
		OTHER PLANTS

TABLE 8 (CONT)

0.00		Omen Name
Cerioalik	Jailk #	TOTAL NATIONAL OPPOSITION OF THE PROPERTY OF THE STATE OF
X51943;	43;	HEPARIN-BINDING GHOWIH FACUOUT FRECONDORON (1905)
[M13361	361;	GROWTH FACTOR) (AFGF) (BE IA-ENDO I HELIAL CELL GROWIN FACTOR) (ECGF.
X65778]	78	BETA).
X53655;	55;	NT-3 (NEUROTROPHIN-3 PRECURSOR) (NEUROTRIC FACTOR) (NEUROTRIC FACTOR)
[M37763	763	GROWTH FACTOR 2) (NGF-2). MACDODIAGE INFLAMMATORY PROTEIN 2-AI PHA [MIP2alpha]
X53/99 V54036	66	黑
X59770	8 6	INTERLEUKIN-1 RECEPTOR TYPE II
X60592	92	CDW40; NERVE GROWTH FACTOR RECEPTOR-RELATED B-LYMPHOCYTE
:		ACTIVATION MOLECULE
X72304	04	CORTICOTROPIN RELEASING FACTOR RECEPTOR
X78686	986	NEUTROPHIL ACTIVATING PROTEIN ENA-78
X79929	53	OX40 LIGAND [gp34]
Y00787	787	8-NIX
Z70519	119	
D17517	517	TYROSINE-PROTEIN KINASE RECEPTOR UFO [sky]
J03241	41	TRANSFORMING GROWTH FACTOR (BETA 3)
J03634	34	INHIBIN BETA (A CHAIN) [activin A, activin AB alpha polypeptide; erythroid differentiation
		protein mRNA (EDF)]
L32976	976	PROTEIN KINASE MLK-3 [MIXED LINEAGE KINASE 1]
L35233	33	AUTOCRINE MOTILITY FACTOR RECEPTOR [AMFR]
M31213;	213;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR (EC
[M57464	7464]	2.7.1.112) (C-RET) [Papillary thyroid carcinoma-encoded protein]
M95489	489	_
005875	875	INTERFERON-GAMMA RECEPTOR BETA CHAIN [Interferon gamma receptor accessory
		factor-1 (AF-1)]
U15979	979;	DELTA-LIKE PROTEIN PRECURSOR (CONTAINS: FETAL ANTIGEN 1) (FA1) (DLK) +
[Z121Z]	172]	ADRENAL SPECIFIC 30kd PROTEIN GB: X17544
X03541	541	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC. 2.7.1.112)
		(TRKT TRANSFORMING TYROSINE NINASE PROTEIN) (P.140-17103) + (IRTS) (P.00-1710) (T.140-17103) + (IRTS) (P.00-1710)
V46040	040	CEL ONLOGENE
V15210	210	CKLEE ATED ONCOGENE SNON
67967X	979	TYROSINE-PROTEIN KINASE CAK [EDDR1; TRK E]
A06925	925	RELAXIN H2
D10232	232	RENIN-BINDING PROTEIN
M13981	3981	INHIBIN ALPHA CHAIN
M31	M31159;	IGFBP3 (GROWTH HORMONE-DEPENDENT INSULIN-LIKE GROWTH FACTOR-BINDING
[M3	[M35878]	PROTEIN)
900	U06863	FOLLISTATIN-RELATED PROTEIN
S85655	655	PROHIBITIN

TABLE 8 (CONT)

	Care Name
delibalin #	Gene wante
D38122;	FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) (APTLGI)
[U08137]	
L11015	
U57059	FAS ANTIGEN LIGAND [TNF-related apoptosis inducing ligand TRAII; Apo-2 ligand]
X14454	INTERFERON REGULATORY FACTOR [Interferon regulatory factor 1]
Y09392;	WSL-LR, WSL-S1, WSL-S2 + TRAMP (Apo-3) (DDR3)
[U75380;U7461	51
1; 083597	TOTOLI TITLE
M27544	INSULIN-LIKE GHOWIH FACTOR IA
M86528	NEUROTROPHIN-4
M86528;	NT-4 (NT-5) + NT-6
S41541;	
[S41540;	
S41522	- 1
U14187	
U14188	RECEPTOR TYROSINE KINASE LIGAND LERK-4 (EPLG4)
U32659	ı
U33635	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR [colon carcinoma kinase-4
	(CCK4)]
U68162	THROMBOPOEITIN RECEPTOR
A25270	IFN-GAMMA ANTAGONIST CYTOKINE
A03911	NEURITE PROMOTING FACTOR(NEXIN), glia derived
D49493	BONE MORPHOGENETIC PROTEIN 3B
D49742;	HGF ACTIVATOR LIKE
[583182]	
L17075	TGF-b superfamily receptor type I (ALK-1) (SRK3)
L03840	FGFR4
L19063	GDNF
L37882	frizzled
L20861	Wnt-5a
M62403	IGFBP4
M65062	IGFBP5
M73980	Notch1
M97016	BONE MORPHOGENETIC PROTEIN 8 (OSTEOGENIC PROTEIN 2)
M99437	notch group protein (N)
U43318	frizzled 5
X07876	WNT2 OR IRP
A26792	CNTF, ISOFORM B AND C
L42379	BPGF-1
271621	Wnt-13
M21626	T CELL RECEPTOR VARIABLE REGION

TABLE 8 (CONT)

	ConBonk #	Gene Name
= -	1182169	frizzled homolog (FZD3)
-	100500	national (mary)
	103300	angupueniri
_	U844U1	smoomened
٦	U90875	cytotoxic ligand TRAIL receptor
٦	U95299	Notch4
×	X91940	WNT-8B
×	X97057	WNT-10B
9	AF003521	Jagged 2
4	AF028593	Jagged 1
	U77493	Notch2
	U94352	manic fringe
	U94354	lunatic fringe
2	M27968	FGF2; HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (PROSTATROPIN). (HBGF-
		2) (BASIC FIBROBLAST GROWTH FACTOR) (BFGF) (PROSTATROPIN)
	L38518	sonic hedgehog (SHH)
-	M60314	BONE MORPHOGENETIC PROTEIN 5
-	M60315	BONE MORPHOGENETIC PROTEIN 6
	M60316	BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1)
	D13365;	GROWTH INHIBITORY FACTOR (METALLOTHIONEIN-III) (MT-III)
-	[M93311]	
	U46010	HGF AGONIST/ANTAGOINST
	L36034	SDF1A (pre-B cell stimulating factor homologue)
	M15530	BCGF1 (B-cell growth factor)
	M58051;	FGFR3 (FLG-2)
	[X58255]	
	M77227	COMPETITIVE HEPATOCYTE GROWTH FACTOR ANTAGONIST. AN ALTERNATIVE
		TRANSCRIPT OF THE HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER
		FACIOR) (SF) (HEPATOPOETTIN A)
	U24163;	frizzled-related FrzB (Fritz) (frezzled (fre))
	[U91903; U680571	
	U28811;	CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR [Golgi membrane
	[U64791]	sialoglycoprotein MG160 (GLG1)}
	U48801;	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) + VEGF
	[U43368]	RELATED FACTOR ISOFORM VRF186 PRECURSOR
	X02492	LEUKOCYTE INTERFERON-INDUCIBLE PEPTIDE
	X85960	trk-T3 (P68 TRK-T3 ONCOPROTEIN)
	X14445	FGF-3; INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH
	10000	FACTOR-3)(HBGF-3).
	M3/625	rar-5, ribhoblasi anowin racion-3 rneconson (ilbar-5).

GenBank	ank #	Gene Name
AF022385	2385	apoptosis-related protein TFAR15 (TFAR15)
L20471	7	extracellular matrix metalloproteinase inducer EMMPRIN
M57730	30	EPHRIN-A1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1)
M37476	9/	(LERK-1) (IMMEDIATE EARLY RESPONSE PROTEIN B61) (TUMOR NECHOSIS FACTOR,
		ALPHA-INDUCED PROTEIN 4).
007695	95	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (17 ROSINE-PROTEIN JANASE BECEPTOR HTK)
1100001	2	EPHRIM.R1 PRECIPEOR (FPH-REI ATED RECEPTOR TYROSINE KINASE LIGAND 2)
) (Seno)	†	(LERK-2) (ELK LIGAND PRECURSOR) (ELK-L).
U82938	38	CD27BP (Siva)
U26403	03	EPHRIN-A5 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 7)
		(LERK-7) (AL-1).
U66406	90	EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8)
VOEADE	30	EPHRIN TYPE A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
7 0 0 0 0	S	KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
		I YROSINE KINASE HEK/).
M62402	102	IGFBP6
AF016268	6268	death receptor 5 (DR5)
AF017986	7986	secreted apoptosis related protein 1
AF017988	7988	secreted apoptosis related protein 3 (SARP3)
L38734	34	EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5)
		(LERK-5) (HTK LIGAND) (HTK-L).
Me3099	99	INTERLEUKIN 1 RECEPTOR AN IAGONISI
L40636	36	EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (1 YROSINE-PROTEIN KINASE RECEPTOR EPH-2) (NET).
1 41030	30	FEMERIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.12) (TYROSINE-PROTEIN EPH-
	9	3) (DRT)
M16591	591	TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK)
		(HEMOPOIETIC CELL KINASE).
M59371	371	EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (1YHOSINE-PHOLEIN
M36395	395	KINASE RECEPTOR ECK) (EPTIMELIAL CELL KINASE).
D14838	838	FGF-9; GLIA-ACTIVATING FACTOR FRECONSON (GAF) (FIBRIOGENS) GINOTATION (FIBRIOGENS) GINOTATION (FIBRIOGENS)
		FACION-9) (TBGF-9).
M77349	349	BIGH3
D25216	216	IGFBP COMPLEX ACID LABILE CHAIN
U36223	223	FGF-8; ANDROGEN-INDUCED GHOW I H FACTOR PRECORSOR (AIGF) (HBGF-8) (FIBROBLAST GROWTH FACTOR-8)
U41745	745	PDGF assoc. protein
U43148	148	patched homolog (PTC)
302958	358	MET

TABLE 8 (CONT)

GenBank #	Gene Name
: !	
1166197	
000101	
X52599	BETANGE
2000	
X52773	retinoic acid receptor alpha (RETINOIC ACID RECEPTOH HXH-ALPHA (HXKA))
2000	A TOLON TO COLUMN TO COLUM
X63454	FGE-6: FIBROBLAST GROWTH FACTOR-6 PRECURSON (HBGF-6) (HST-2).
1000	
X65923	EAU
2000	

Cell Cycle Array

In the cell cycle array according to the subject invention, all of the unique polynucleotide probe compositions correspond to genes that are associated with the life cycle of a cell. In a specific cell cycle array of interest, the spots are as provided in Table 9.

TABLE 9

	ConBont #	Gono Namo
	ב אוופסווס	
		MDMZ PROTEIN (P53-ASSOCIATED PROTEIN) + MDMZ-A (GB: U33199) + MDM2-C (GB:
	Z12020; [M92424]	U33201)
	M14694; [M14695]	p53
	U18422	DP2 (Humdp2), dimerization partner of E2F
		DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE (INASE 1 (EC. 2.7.1.) (MAP) KINASE KINASE 1) (MAPKK 1) JERK ACTIVATOR KINASE 1, MARKIERK KINASE 1
	L05624	(MEXI).
	L07540	ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (RFC36)
	L07541	ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (RFC38)
		CELL DIVISION PROTEIN KINASE 7 (EC 2.7.1) (CDK-ACTIVATING KINASE) (CAK) (39
	L20320	KD PROTEIN KINASE) (P39 MO15) (STK1) (CAK1).
	L29511: [M96995]	GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTOR PROTEIN) (ASH PROTEIN).
	L33264	CDC2-RELATED KINASE PISSLRE
		REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION
	M63488	PACTOR: A PROTEIN 1) (SINGLE STRANDED DNA-BINDING PHOTEIN)
	M74524	HHREA (YEAST RADE HOMOLOG) (UBIQITIN-CONJUGATING ENZYME) (UBCA)
	M87338	ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (RFC40)
	M87339	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (RFC37)
		CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION
		ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INTERACTING PROTEIN 1) (CIP1)
	U09579; [L25610]	(WAF1) (CDKN1A) (CDKN1) (SDI1) (PIC1) (CAP20)
	M68520	CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.) (P33 PROTEIN KINASE)
	MB1933	cdc25A; M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48)
	M92287	CYCLIN D3
	M96684	TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA
	X51688	CYCLIN A
	X03484	RAF ONCOGENE
-	X59798; [M64349]	CYCLIN D1 (CYCLIN PRAD1) (BCL-1 ONCOGENE)
	D13639 [M90813]	CYCLIN D2
	HT3218 [K00065]	SUPEROXIDE DISMUTASE [Superoxide dismutase 1 (Cu/Zn)]
		UV EXCISION REPAIR PROTEIN PROTEIN RAD23 [xeroderma pigmentosum group C
	D21235	repair complementing protein HHR23A]
	U11791 [U12685]	CYCLIN H
	L26318	STRESS-ACTIVATED PROTEIN KINASE JNK1 (EC 2.7.1) (C-JUN N-TERMINAL KINASE 1) (JNK-46)
	L27211	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1), (CDKN2A)
		1

Ancard.	Gone Name
	ACTIVITY OF ACTIVITY OF DESCRIPTION WAS DE DOG (FC 0.7.4.) MAD WHACE DOG (CVTOVINE
	SUPPRESSIVE ANTHINELAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING
 L35253; [L35263]	PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2).
M13228	N-myc
M15400	Retinoblastoma susceptibility (RB1 retinoblastoma-assoc)
M25753	CYCLIN B1 G2MITOTIC-SPECIFIC
	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (DNA-DAMAGE
M00374	CYCLIN F
	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE
540/05 [552138]	INDUCIDLE FROITEMY (CHOT).
U40343; [U20498]	CYCLIN-DEPENDEN! KINASE 4 INHIBITION D (PT9-INK4D).
U47413 [L49504]	CYCLIN G1
U47414 [L49506]	CYCLIN G2
	EXTRACELLULAR SIGNAL-REGULATED KINASE 1 (EC 2.7.1) (ERK1) (INSULIN-
X60188	(MICROTUBULE-ASSOCIATED PROTEIN-2 KINASE).
	EXTRACELLULAR SIGNAL-REGULATED KINASE 3 (EC 2.7.1) (ERK3) (MAP KINASE
X80692	ISOFORM P97) (P97-MAPK).
131051	STRESS-ACTIVATED PROTEIN KINASE JNK2 (EC 2.7.1) (C-JUN N-TERMINAL KINASE
L31931	2) (UNIV. 2007).
U34819; [U07620]	STRESS-ACTIVATED PHOLEIN KINASE JNK3 (EC 2.7.1) (C-JUN N-LEHMINAL KINASE 3) (JNK3) (MAP KINASE P49 3F12).
129216	CLK-2
L29220	CLK:3
L29222	CLK-1
U10564	WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112) (Wee1Hu)
U22398	CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR PS7) (PS7KIP2)
U33841	ATAXIA TELANGIECTASIA (ATM)
1130657	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 6 (EC 2.7.1) (MAPINASE 6) (MAPIKK 6) (MAPIKKENASE 6) (SAPKK3)
M81934: [S78187]	cdc25B: M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). (CDC25Hu2)
	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2) (CDKN2B).
X74262	ВВА/р48
X85133	RBQ1 retinoplastoma binding protein
X85753	CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1) (PROTEIN KINASE K35).

	# 11-00	
	Genbank #	Gene Name
-	L13698	GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1).
7	D63878	NEDD5 PROTEIN HOMOLOG.
	L23959	E2F-related transcription factor (DP-1)
	L25676	SERINE/THREONINE PROTEIN KINASE PITALRE
	M14505	CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1) (PSK-J3)
	M29039	Jun B TRANSACTIVATOR
-	M34065	cdc25C; M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).
	M35543; [M57298]	cdc42 homolog (G25K) [brain isoform + placental isoform]
	L22005	UBIQUITIN-CONJUGATING ENZYME E2-CDC34
	M95712	raf,b-
	S72008	CDC10 PROTEIN HOMOLOG
	U15642	E2F-5
	U24152	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1) (P65-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK)
	U24153	p21-activated protein kinase (Pak2)
		EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1) (ERK5) (ERK4) (BMK1
	U25278	KINASE)
	U34051	CYCLIN-DEPENDENT KINASE 5 ACTIVATOR ISOFORM P39I PRECURSOR (CDK5 ACTIVATOR) (P39I).
		MITOGEN-ACTIVATED PROTEIN KINASE P38 BETA (EC 2.7.1) (MAP KINASE P38
	U53442	BETA)
	L34075	FKBP-RAPAMYSIN ASSOCIATED PROTEIN (FRAP)
	X05360	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1)
	L40027	glycogen synthase kinase 3
	X59727	EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK).
	X66360	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2
	X66362	SERINE/THREONINE PROTEIN KINASE PCTAIRE-3
	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1
	X66364	CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE).
	X66365	CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1) (KINASE PLSTIRE)
	X74594	RB2/p130
	X79483	EXTRACELLULAR SIGNAL-REGULATED KINASE 6 (EC 2.7.1) (ERK6) (ERK5)

TABLE 9 (CONT)

# 21.00	Cons Name
Gendank #	מפופ אמווס
	CYCLIN-DEPENDENT KINASE 5 ACTIVATOR PRECURSOR (CDK5 ACTIVATOR) (TAU PROTEIN KINASF II 23 KD SUBUNIT) (TPKII REGULATORY SUBUNIT) (P23) (P25).
X85134	RBO:3
M15796; [J04718]	PCNA (CYCLIN)
AF001954	growth inhibitor p33ING1 (ING1)
AF007111	MDM2-like p53-binding protein (MDMX)
D89667	C-myc binding protein
U66469	p53-dependent cell growth regulator CGR19
U77949	CDC6-RELATED PROTEIN
U78876	MEK KINASE 3
Y11416	p73, a monoallelically expressed p53-related protein
Y10479	E2F-3
U02570	CDC42 GTPase-activating protein
	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 2 (EC 2.7.1)
L11285	(MAP KINASE KINASE Z) (MAPRIN Z) (ERN ACTIVATION RIMASE Z) (WAITED STANDED Z) (MEK2).
M63167	Akt1 (rac protein kinase alpha, protein kinase B, c-Akt)
S57153: S57160	RBP1(RETINOBLASTOMA-BINDING PROTEIN)
U23435; U31089	Abl interactor 2 (Abi-2) + Abl binding protein 3 (AbIBP3) [ArgBPIB]
	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (RAS-LIKE PROTEIN
 M29870; [M31467]	TC25)
M96577	E2F-1 pRB-binding protein
230301	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5 (EC 2.7.1) (MAPI KINASE KINASE 5) (MAPKK 5) (MAPKERK KINASE 5).
X66357	CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1).
M74091	CYCLIN C G1/S-SPECIFIC
M80629	CDC2-RELATED PROTEIN KINASE CHED
S66431	RBP2 retinoblastoma binding protein
 U00001	CDC27HS PROTEIN
U01038	SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1) (PLK-1) (STPK13)
D50310	CYCLIN I
U18291	CDC16HS.
U63131	CDC37 HOMOLOG.
U69276	GRB-IR / GRB10
X66358	SERINE/THREONINE-PROTEIN KINASE KKIALRE

Other Representative Arrays

In a neuroarray according to the subject invention, all of the unique polynucleotide probe compositions will correspond to genes that are expressed in brain related tissues. Genes that are represented on the array are key genes, by which is meant that they have been reported to play primary roles in a variety of different biological processes in brain tissues. Genes of interest that may be represented on the array include: ion channel/transport proteins; receptors; cell cycle regulators; stress response proteins; apoptosis proteins; signal transduction proteins; transcriptional factors; growth factors/interleukins/hormones; oncogenes and tumor suppressors; cell surface/adhesion proteins; DNA synthesis/repair/recombination genes; and metabolic pathway enzymes.

In certain embodiments, of particular interest is an array having the following types of genes represented on its surface: nuclear proteins; endoplasmic reticulum proteins; golgi complex proteins; endosomal proteins; lysosomal proteins; peroxisomal proteins; mitochondrial proteins; cytoplasmic proteins; cytoskeletal proteins; plasma membrane proteins; post synaptic and dendritic proteins; axonal and nerve terminal proteins; secreted proteins, neuropeptides, hormones and growth factors; extracellular matrix proteins; astrocyte and oligodendroglial proteins; immune system proteins; developmentally regulated proteins; regionally regulated proteins; and disease related proteins.

Other representative arrays include: (1) rat arrays, in which each of the unique polynucleotide corresponds to a key rat gene; (2) blood arrays, in which each unique polynucleotide corresponds to a gene associated cells and tissues associated with the cardiovascular system; (3) rat stress arrays; and (4) mouse stress arrays, in which each unique polynucleotide corresponds to a gene associated with the stress response of murine cells.

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METHODS OF USING THE SUBJECT ARRAYS

The subject arrays find use in a variety of different applications in which one is interested in detecting the occurrence of one or more binding events between target nucleic acids and probes on the array and then relating the occurrence of the binding event(s) to the presence of a target(s) in a sample. In general, the device will be contacted with the sample suspected of containing the target under conditions sufficient for binding of any target

present in the sample to a complementary polynucleotide present on the array. Generally, the sample will be a fluid sample and contact will be achieved by introduction of an appropriate volume of the fluid sample onto the array surface, where introduction can be pipette, deposition, and the like.

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Generation of Labeled Target

Targets may be generated by methods known in the art. mRNA can be labeled and used directly as a target, or converted to a labeled cDNA target. Generally, such methods include the use of oligonucleotide primers. Primers that may be employed include oligo dT, random primers, e.g. random hexamers and gene specific primers.

Of particular interest in the generation of labeled target is the use of a set of a representational number of gene specific primers, as described in U.S. Patent Application No. 08/859,998, the disclosure of which is herein incorporated by reference. As the subject sets comprise a representational number of primers, the total number of different primers in any given set will be only a fraction of the total number of different or distinct RNAs in the sample, where the total number of primers in the set will generally not exceed 80 %, usually will not exceed 50 % and more usually will not 20% of the total number of distinct RNAs, usually the total number of distinct messenger RNAs (mRNAs), in the sample. Any two given RNAs in a sample will be considered distinct or different if they comprise a stretch of at least 100 nucleotides in length in which the sequence similarity is less than 98%, as measured using the FASTA algorithm at default settings. As the sets of gene specific primers comprise only a representational number of primers, with physiological sources comprising from 5,000 to 50,000 distinct RNAs, the number of different gene specific primers in the set of gene specific primers will typically range from about 20 to 10,000, usually from 50 to 2,000 and more usually from 75 to 1500.

Each of the gene specific primers of the sets described above will be of sufficient length to specifically hybridize to a distinct nucleic acid member of the sample, e.g. RNA or c DNA, where the length of the gene specific primers will usually be at least 8 nt, more usually at least 20 nt and may be as long as 25 nt or longer, but will usually not exceed 50 nt. The gene specific primers will be sufficiently specific to hybridize to complementary template sequence during the generation of labeled nucleic acids under conditions sufficient for first strand cDNA synthesis, which conditions are known by those of skill in the art. The

number of mismatches between the gene specific primer sequences and their complementary template sequences to which they hybridize during the generation of labeled nucleic acids in the subject methods will generally not exceed 20 number %, usually will not exceed 10 number % and more usually will not exceed 5 number %.

Generally, the sets of gene specific primers will comprise primers that correspond to at least 20, usually at least 50 and more usually at least 75 distinct genes as represented by distinct mRNAs in the sample, where the term "distinct" when used to describe genes is as defined above, where any two genes are considered distinct if they comprise a stretch of at least 100 nt in their RNA coding regions in which the sequence similarity does not exceed 98%, as determined using the FASTA algorithm at default settings.

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The gene specific oligonucleotide primers may be synthesized by conventional oligonucleotide chemistry methods, where the nucleotide units may be: (a) solely nucleotides comprising the heterocyclic nitrogenous bases found in naturally occurring DNA and RNA, *e.g.* adenine, cytosine, guanine, thymine and uracil; (b) solely nucleotide analogs which are capable of base pairing under hybridization conditions in the course of DNA synthesis such that they function as the above nucleotides found in naturally occurring DNA and RNA, where illustrative nucleotide analogs include inosine, xanthine, hypoxanthine, 1,2-diaminopurine and the like; or (c) from combinations of the nucleotides of (a) and nucleotide analogs of (b), where with primers comprising a combination of nucleotides and analogues thereof, the number of nucleotide analogues in the primers will typically be less than 25 and more typically less than 5. The gene specific primers may comprise reporter or hapten groups, usually 1 to 2, which serve to improve hybridization properties and simplify detection procedure.

Depending on the particular point at which the gene specific primers are employed in the generation of the labeled nucleic acids, *e.g.* during first strand cDNA synthesis or following one or more distinct amplification steps, each gene specific primer may correspond to a particular RNA by being complementary or similar, where similar usually means identical, to the particular RNA. For example, where the gene specific primers are employed in the synthesis of first strand cDNA, the gene specific primers will be complementary to regions of the RNAs to which they correspond.

Each gene specific primer can be complementary to a sequence of nucleotides which is unique in the population of nucleic acids, e.g. mRNAs, with which the primers are

contacted, or one or more of the gene specific primers in the set may be complementary to several nucleic acids in a given population, *e.g.* multiple mRNAs, such that the gene specific primer generates labeled nucleic acid when one or more of set of related nucleic acid species, *e.g.* species having a conserved region to which the primer corresponds, are present in the sample. Examples of such related nucleic acid species include those comprising: repetitive sequences, such as Alu repeats, Al repeats and the like; homologous sequences in related members of a gene-family; polyadenylation signals; splicing signals; or arbitrary but conversed sequences.

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Depending on the particular nature of the labeled nucleic acid generation step of the subject methods, the gene specific primers may be modified in a variety of ways. One way the gene specific primers may be modified is to include an anchor sequence of nucleotides, where the anchor is usually located 5' of the gene specific portion of the primer and ranges in length from 10 to 50 nt in length, usually 15 to 40 nt in length. The anchor sequence may comprise a sequence of bases which serves a variety of functions, such as a sequence of bases which correspond to the sequence found in promoters for bacteriophage RNA polymerase, *e.g.* T7 polymerase, T3 polymerase, SP6 polymerase, and the like; arbitrary sequences which can serve as subsequent primer binding sites; and the like.

Turning now to the methods employing the above sets of gene specific primers, the first step in the subject methods is to obtain a sample of nucleic acids, usually RNAs, from a physiological source, usually a plurality of physiological sources, where the term plurality is used to refer to 2 or more distinct physiological sources. The physiological source of RNAs will typically be eukaryotic, with physiological sources of interest including sources derived single celled organisms such as yeast and multicellular organisms, including plants and animals, particularly mammals, where the physiological sources from multicellular organisms may be derived from particular organs or tissues of the multicellular organism, or from isolated cells derived therefrom. Thus, the physiological sources may be different cells from different organisms of the same species, *e.g.* cells derived from different humans, or cells derived from the same human (or identical twins) such that the cells share a common genome, where such cells will usually be from different tissue types, including normal and diseased tissue types, *e.g.* neoplastic, cell types. In obtaining the sample of RNAs to be analyzed from the physiological source from which it is derived, the physiological source may be subjected to a number of different processing steps, where such processing steps

might include tissue homogenation, nucleic acid extraction and the like, where such processing steps are known to the those of skill in the art. Methods of isolating RNA from cells, tissues, organs or whole organisms are known to those of skill in the art and are described in Maniatis *et al.*, Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Press)(1989).

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The next step in the subject methods is the generation of labeled nucleic acids representative of the nucleic acid, usually RNA, profile of the physiological source. As mentioned above, a set of gene specific primers is used to generate the labeled nucleic acids from the sample of RNAs, where the labeled nucleic acids generated in this step may serve as "target" in subsequent assays in which the differences in the RNA profiles of at least two sources are analyzed. As used herein, the term "target" refers to single stranded RNA, single stranded DNA and double stranded DNA, where the target is generally greater than 50 nt in length.

The set of primers may be used either in first strand cDNA synthesis or following one or more amplification steps. Furthermore, the actual synthesis of the labeled nucleic acids may be at the same step during which the sets of gene specific primers are employed, or the synthesis of the labeled nucleic acids may be one more steps subsequent to the step in which the sets of gene specific primers are employed.

In a first embodiment of the invention, the set of gene specific primers is used to generate labeled first strand cDNA, where the labeled first strand cDNA is representative of the RNA profile of the physiological source being assayed. The labeled first strand cDNA is prepared by contacting the RNA sample with the primer set and requisite reagents under conditions sufficient for reverse transcription of the RNA template in the sample. Requisite reagents contacted with the primers and RNAs are known to those of skill in the art and will generally include at least an enzyme having reverse transcriptase activity and dNTPs in an appropriate buffer medium.

A variety of enzymes, usually DNA polymerases, possessing reverse transcriptase activity can be used for the first strand cDNA synthesis step. Examples of suitable DNA polymerases include the DNA polymerases derived from organisms selected from the group consisting of a thermophilic bacteria and archaebacteria, retroviruses, yeasts, Neurosporas, Drosophilas, primates and rodents. Preferably, the DNA polymerase will be selected from the group consisting of Moloney murine leukemia virus (M-MLV) as described in United

States Patent No. 4,943,531 and M-MLV reverse transciptase lacking RNaseH activity as described in United States Patent No. 5,405,776 (the disclosures of which patents are herein incorporated by reference), human T-cell leukemia virus type I (HTLV-I), bovine leukemia virus (BLV), Rous sarcoma virus (RSV), human immunodeficiency virus (HIV) and Thermus aquaticus (Taq) or Thermus thermophilus (Tth) as described in United States Patent No. 5,322,770, the disclosure of which is herein incorporated by reference. Suitable DNA polymerases possessing reverse transcriptase activity may be isolated from an organism, obtained commercially or obtained from cells which express high levels of cloned genes encoding the polymerases by methods known to those of skill in the art, where the particular manner of obtaining the polymerase will be chosen based primarily on factors such as convenience, cost, availability and the like.

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The various dNTPs and buffer medium necessary for first strand cDNA synthesis through reverse transcription of the primed RNAs may be purchased commercially from various sources, where such sources include Clontech, Sigma, Life Technologies, Amersham, Boehringer-Mannheim. Buffer mediums suitable for first strand synthesis will usually comprise buffering agents, usually in a concentration ranging from 10 to 100 μM which typically support a pH in the range 6 to 9, such as Tris-HCl, HEPES-KOH, etc.; salts containing monovalent ions, such as KCl, NaCl, etc., at concentrations ranging from 0-200 mM; salts containing divalent cations like MgCl₂, Mg(OAc) etc, at concentrations usually ranging from 1 to 10 mM; and additional reagents such as reducing agents, e.g. DDT, detergents, albumin and the like. The conditions of the reagent mixture will be selected to promote efficient first strand synthesis. Typically the set of primers will first be combined with the RNA sample at an elevated temperature, usually ranging from 50 to 95 °C, followed by a reduction in temperature to a range between about 0 to 60°C, to ensure specific annealing of the primers to their corresponding RNAs in the sample. Following this annealing step, the primed RNAs are then combined with dNTPs and reverse transcriptase under conditions sufficient to promote reverse transcription and first strand cDNA synthesis of the primed RNAs. By using appropriate types of reagents, all of the reagents can be combined at once if the activity of the polymerase can be postponed or timed to start after annealing of the primer to the RNA.

In this embodiment, one of either the gene specific primers or dNTPs, preferably the dNTPs, will be labeled such that the synthesized cDNAs are labeled. By labeled is meant

that the entities comprise a member of a signal producing system and are thus detectable, either directly or through combined action with one or more additional members of a signal producing system. Examples of directly detectable labels include isotopic and fluorescent moieties incorporated into, usually covalently bonded to, a nucleotide monomeric unit, e.g. dNTP or monomeric unit of the primer. Isotopic moieties or labels of interest include 32P, ³³P, ³⁵S, ¹²⁵I, and the like. Fluorescent moieties or labels of interest include coumarin and its derivatives, e.g. 7-amino-4-methylcoumarin, aminocoumarin, bodipy dyes, such as Bodipy FL, cascade blue, fluorescein and its derivatives, e.g. fluorescein isothiocyanate, Oregon green, rhodamine dyes, e.g. texas red, tetramethylrhodamine, eosins and erythrosins, cyanine dyes, e.g. Cy3 and Cy5, macrocyclic chelates of lanthanide ions, e.g. quantum dye™, fluorescent energy transfer dyes, such as thiazole orange-ethidium heterodimer, TOTAB, etc. Labels may also be members of a signal producing system that act in concert with one or more additional members of the same system to provide a detectable signal. Illustrative of such labels are members of a specific binding pair, such as ligands, e.g. biotin, fluorescein, digoxigenin, antigen, polyvalent cations, chelator groups and the like, where the members specifically bind to additional members of the signal producing system, where the additional members provide a detectable signal either directly or indirectly, e.g. antibody conjugated to a fluorescent moiety or an enzymatic moiety capable of converting a substrate to a chromogenic product, e.g. alkaline phosphatase conjugate antibody; and the like.

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In one preferred embodiment, the member of the signal producing system bound to the nucleotide is functional group capable of covalently binding to additional members of the signal producing system to generate a detectable label. Examples of such functional groups or moieties include amino, sulfhydryl, azido, isothiocyanate, sulfoxyl, and the like. The labeled target generated using such nucleotides will thus include one or more, usually a plurality of, functional moieties. For detection, the functional moieties of the modified nucleotides can be labeled by conjugation of a label to the functional moiety. A variety of suitable labels and methods for their conjugation to functional moieties are known to those of skill in the art. Examples include labeling of amino-modified cDNA by a succinimidyl ester of an appropriate dye, e.g. Alexa, Bodipy, or Cy dyes. Alternatively, label can be entrapped or bonded into structures of microscopic-sized particles. These particles can then be conjugated with the functional moieties of the target.

For each sample of RNA, one can generate labeled oligos with the same labels. Alternatively, one can use different labels for each physiological source, which provides for additional assay configuration possibilities, as described in greater detail below.

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In a variation of the above embodiment, where desired one can generate labeled RNA instead of labeled first strand cDNA. In this embodiment, first strand cDNA synthesis is carried out in the presence of unlabeled dNTPs and unlabeled gene specific primers. However, the primers are optionally modified to comprise a promotor for an RNA polymerase, such as T7 RNA polymerase, T3 RNA polymerase, SP6 RNA polymerase, and the like. In this embodiment, following first strand cDNA synthesis, the resultant single stranded cDNA is then converted to double stranded cDNA, where the resultant double stranded cDNA comprises the anchor sequence comprising the promoter region. Conversion of the mRNA:cDNA hybrid following first strand synthesis can be carried out as described in Okayama & Berg, Mol. Cell. Biol. (1982) 2:161-170, and Gubler & Hoffman, Gene (1983) 25: 253-269, where briefly the RNA is digested with a ribonuclease, such as E.coli RNase H, followed by repair synthesis using a DNA polymerase like DNA polymerase I, etc., and E.coli DNA ligase. One may also employ the modification of this basic method described in Wu, R, ed., Methods in Enzymology (1987), vol. 153 (Academic Press). Next, the double stranded cDNA is contacted with RNA polymerase and dNTPs, including labeled dNTPs as described above, to produce linearly amplified labeled ribonucleic acids. For cDNA lacking the anchor sequence comprising a promoter region, a polymerase that does not need a promoter region but instead can initiate RNA strand synthesis randomly from cDNA, such as core fragment of E.Coli RNA polymerase, may be employed.

In another embodiment of the subject invention, the labeled nucleic acid generation step comprises one or more enzymatic amplification steps in which multiple DNA copies of the initial RNAs present in the sample are produced, from which multiple copies of the initial RNA or multiple copies of antisense RNA (aRNA) may be produced, using the polymerase chain reaction, as described in U.S. Pat. No. 4,683,195, the disclosure of which is herein incorporated by reference, in which repeated cycles of double stranded DNA denaturation, oligonucleotide primer annealing and DNA polymerase primer extension are performed, where the PCR conditions may be modified as described in U.S. Pat No. 5,436,149, the disclosure of which is herein incorporated by reference.

In one embodiment involving enzymatic amplification, the set of gene-specific primers are employed in the generation of the first strand cDNA, followed by amplification of the first strand cDNA to produce amplified numbers of labeled cDNA. In this embodiment, as a set of gene-specific primers is employed in the first strand synthesis step, only a representative proportion of the total RNA in the sample is amplified during the subsequent amplification steps.

Amplification of the first strand cDNA can be conveniently achieved by using a CAPswitchTM oligonucleotide as described in U.S. Patent Application Serial No. 08/582,562, the disclosure of which is herein incorporated by reference. Briefly, the CAPswitchTM technology uses a unique CAPswitchTM oligonucleotide in the first strand cDNA synthesis followed by PCR amplification in the second step to generate a high yield of ds cDNA. When included in the first-strand cDNA synthesis reaction mixture, the CAPswitchTM oligonucleotide serves as a short extended template. When reverse transcriptase stops at the 5' end of the mRNA template in the course of first strand cDNA synthesis it switches templates and continues DNA synthesis to the end of the CAPswitchTM oligonucleotide. The resulting ss cDNA incorporates at the 3' end, sequence which is complimentary to complete 5' end of the mRNA and the CAPswitchTM oligonucleotide sequence.

Of particular interest as the CAPswitchTM oligonucleotide are oligonucleotides having the following formula:

5'-dN1-dN2-...dNm-rN1-rN2...rNn-3'

wherein:

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dN represents a deoxyribonucleotide selected from among dAMP, dCMP, dGMP and dTMP;

m represents an integer 0 and above, preferably from 10 to 50;

rN represents a ribonucleotide selected from the group consisting of AMP, CMP, GMP and UMP, preferably GMP; and

n represents an integer 0 and above, preferably from 3 to 7.

The structure of the CAPswitch™ oligonucleotide may be modified in a number of ways, such as by replacement of 1 to 10 nucleotides with nucleotide analogs, incorporation

of terminator nucleotides, such as 3'-amino NMP, 3'-phosphate NMP and the like, or non-natural nucleotides which can improve efficiency of the template switching reaction but still retain the main function of the CAPswitchTM oligonucleotide *i.e.* CAP-depended extension of full-length cDNA by reverse transcriptase using CAPswitchTM oligonucleotide as a template.

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In using the CAPswitch™ oligonucleotide, first strand cDNA synthesis is carried out in the presence of a set of gene specific primers and a CAPswitchTM oligonucleotide, where the gene specific primers have been modified to comprise an arbitrary anchor sequence at their 5' ends. The first strand cDNA is then combined with primer sequences complementary to: (a) all or a portion of the CAPswitchTM oligonucleotide and (b) the arbitrary anchor sequence of the gene specific primers and additional PCR reagents, such as dNTPs, DNA polymerase, and the like, under conditions sufficient to amplify the first strand cDNA. Conveniently, PCR is carried out in the presence of labeled dNTPs such that the resultant, amplified cDNA is labeled and serves as the labeled or target nucleic acid. Labeled nucleic acid can also be produced by carrying out PCR in the presence of labeled primers, where either or both the CAPswitchTM oligonucleotide complementary primer and anchor sequence complementary primer may be labeled. In yet an alternative embodiment, instead of producing labeled amplified cDNA, one may generate labeled RNA from the amplified ds cDNA, e.g. by using an RNA polymerase such as E.coli RNA polymerase, or other RNA polymerases requiring promoter sequences, where such sequences may be incorporated into the arbitrary anchor sequence.

Instead of using the set of gene specific primers in the first strand cDNA synthesis step followed by subsequent amplification of only a representative fraction of the total number of distinct RNA species in the sample, one may also amplify all of the RNAs in the sample and use the set of gene specific primers to generate labeled nucleic acid following amplification. This embodiment may find use in situations where the RNA of interest to be amplified is known or postulated to be in small amounts in the sample.

In this embodiment, first strand synthesis is carried out using: (a) an oligo dT primer that usually comprises an arbitrary anchor sequence at its 5' end and (b) a CAPswitchTM oligonucleotide. During first strand synthesis the oligo(dT) anneals to the polyA tail of the mRNA in the sample and synthesis extends beyond the 3' end of the RNA to include the CAPswitchTM oligonucleotide, yielding a first strand cDNA comprising an arbitrary

sequence at its 5' end and a region complementary to the CAPswitchTM oligonucleotide at its 3' end. The length of the dT primer will typically range from 15 to 30 nts, while the arbitrary anchor sequence or portion of the primer will typically range from 15 to 25 nt in length.

Following first strand synthesis, the cDNA is amplified by combining the first strand cDNA with primers that correspond at least partially to the anchor sequence and the CAPswitchTM oligonucleotide under conditions sufficient to produce an amplified amount of the cDNA. Labeled nucleic acid is then produced by contacting the resultant amplified cDNA with a set of gene specific primers, a polymerase and dNTPs, where at least one of the gene specific primers and dNTPs are labeled.

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When employed to generate target, as described above, the gene specific primers of the sets of primers according to the subject invention are typically chosen according to a number of different criteria. In some embodiments of the invention, primers of interest for inclusion in the set include primers corresponding to genes which are typically differentially expressed in different cell types, in disease states, in response to the influence of external agents, factors or infectious agents, and the like. In other embodiments, primers of interest are primers corresponding to genes which are expected to be, or already identified as being, differentially expressed in different cell, tissue or organism types. Preferably, at least 2 different gene functional classes will be represented in the sets of gene specific primers, where the number of different functional classes of genes represented in the primer sets will generally be at least 3, and will usually be at least 5. Gene functional classes of interest include oncogenes; genes encoding tumor suppressors; genes encoding cell cycle regulators; stress response genes; genes encoding ion channel proteins; genes encoding transport proteins; genes encoding intracellular signal transduction modulator and effector factors; apoptosis related genes; DNA synthesis/recombination/repair genes; genes encoding transcription factors; genes encoding DNA-binding proteins; genes encoding receptors, including receptors for growth factors, chemokines, interleukins, interferons, hormones, neurotransmitters, cell surface antigens, cell adhesion molecules etc.; genes encoding cellcell communication proteins, such as growth factors, cytokines, chemokines, interleukins, interferons, hormones etc.; and the like. Less preferred are gene specific primers that are subject to formation of strong secondary structures with less than -10kcal/mol; comprise stretches of homopolymeric regions, usually more than 5 identical nucleotides; comprise

more than 3 repetitive sequences; have high, e.g. more than 80%, or low, e.g. less than 30%, GC content etc.

The particular genes represented in the set of gene specific primers will necessarily depend on the nature of physiological source from which the RNAs to be analyzed are derived. For analysis of RNA profiles of eukaryotic physiological sources, the genes to which the gene specific primers correspond will usually be Class II genes which are transcribed into RNAs having 5' caps, *e.g.* 7-methyl guanosine or 2,2,7-trimethylguanosine, where Class II genes of particular interest are those transcribed into cytoplasmic mRNA comprising a 7-methyl guanosine 5' cap and a polyA tail.

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For analysis of RNA profiles of mammalian physiological sources, of particular interest are gene specific primers corresponding to the functional gene classes listed above. For analysis of RNA profiles of human physiological sources, the gene specific primers of particular interest are the gene specific primers identified in Table 1 as SEQ ID NO:01 to SEQ ID NO:1372, of U.S. Application Serial No. 08/859,998, the disclosure of which is herein incorporated by reference, where sets of these primers will usually include at least 20 and more usually at least 50 of these specific sequences.

Particular sets of primers of interest in the subject invention are those sets of primers that include primers capable of amplifying at least a portion of the unique polynucleotides present on the arrays with which the target is to be employed. By at least a portion is meant at least about 10, usually at least about 20 and more usually at least about 25 number % (where number is the number of different unique polynucleotides on the array). For examples, sets of primers that include primers capable of amplifying at least a portion of the unique polynucleotides listed in Table 1, *supra*, are of interest. Similarly sets of primers capable of amplifying at least a portion of the unique polynucleotides listed in Tables 2 to 8, *supra*, are also of interest.

In a particularly preferred embodiment, the gene specific primers are preferably those primers that correspond to the different polynucleotide spots on the array that is used in the hybridization assay. Thus, one will preferably employ gene specific primers for each different polynucleotide that is present on the array, so that if the gene is expressed in the particular cell or tissue being analyzed, labeled target will be generated from the sample for that gene. In many embodiments in which the subject arrays are employed, the gene specific primers used to generate the target from the human cell or tissue being analyzed will have

the same sequence as the gene specific primers used to generate the polynucleotide probes present on the array. In this manner, if a particular gene present on the array is expressed in a particular sample, the appropriate target will be generated and subsequently identified.

Representative sets of primers falling within this particularly preferred embodiment include:

5	SET	DESCRIPTION
	1	I pair of primers capable of amplifying each polynucleotide listed in Table 1, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 1.
	2	I pair of primers capable of amplifying each polynucleotide listed in Table 2, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 2.
	3	l pair of primers capable of amplifying each polynucleotide listed in Table 3, <i>supra</i> , as well one set of primers capable of amplifying each of the complementary sequences of each of the polynucleotides listed in Table 3.

10 Hybridization and Detection

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As mentioned above, following preparation of the target nucleic acid from the tissue or cell of interest, the target nucleic acid is then contacted with the array under hybridization conditions, where such conditions can be adjusted, as desired, to provide for an optimum level of specificity in view of the particular assay being performed. Suitable hybridization conditions are well known to those of skill in the art and reviewed in Maniatis et al, *supra* and WO 95/21944. In analyzing the differences in the population of labeled target nucleic acids generated from two or more physiological sources using the arrays described above, each population of labeled target nucleic acids are separately contacted to identical probe arrays or together to the same array under conditions of hybridization, preferably under stringent hybridization conditions (for example, at 50°C or higher and 0.1XSSC (15 mM sodium chloride/01.5 mM sodium citrate)), such that labeled target nucleic acids hybridize to complementary probes on the substrate surface.

Where all of the target sequences comprise the same label, different arrays will be employed for each physiological source (where different could include using the same array at different times). Alternatively, where the labels of the targets are different and

distinguishable for each of the different physiological sources being assayed, the opportunity arises to use the same array at the same time for each of the different target populations. Examples of distinguishable labels are well known in the art and include: two or more different emission wavelength fluorescent dyes, like Cy3 and Cy5, two or more isotopes with different energy of emission, like ³²P and ³³P, labels which generate signals under different treatment conditions, like temperature, pH, treatment by additional chemical agents, etc., or generate signals at different time points after treatment. Using one or more enzymes for signal generation allows for the use of an even greater variety of distinguishable labels, based on different substrate specificity of enzymes (alkaline phosphatase/peroxidase).

Following hybridization, non-hybridized labeled nucleic acid is removed from the support surface, conveniently by washing, generating a pattern of hybridized nucleic acid on the substrate surface. A variety of wash solutions are known to those of skill in the art and may be used.

The resultant hybridization patterns of labeled nucleic acids may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the target nucleic acid, where representative detection means include scintillation counting, autoradiography, fluorescence measurement, colorimetric measurement, light emission measurement and the like.

Following detection or visualization, the hybridization patterns may be compared to identify differences between the patterns. Where arrays in which each of the different probes corresponds to a known gene are employed, any discrepancies can be related to a differential expression of a particular gene in the physiological sources being compared.

Utility

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The subject methods find use in, among other applications, differential gene expression assays. Thus, one may use the subject methods in the differential expression analysis of: (a) diseased and normal tissue, e.g. neoplastic and normal tissue, (b) different tissue or tissue types; (c) developmental stage; (d) response to external or internal stimulus; (e) response to treatment; and the like. The subject arrays therefore find use in broad scale expression screening for drug discovery and research, such as the effect of a particular active agent on the expression pattern of genes in a particular cell, where such information can be

used to reveal drug toxicity, carcinogenicity, etc., environmental monitoring, disease research and the like.

Kits

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Also provided are kits for performing analyte binding assays using the subject devices, where kits for carrying out differential gene expression analysis assays are preferred. Such kits according to the subject invention will at least comprise the subject arrays. The kits may further comprise one or more additional reagents employed in the various methods, such as primers for generating target nucleic acids, including a set of gene specific primers according to the subject invention, e.g. primer sets 1 to 9 described above, dNTPs and/or rNTPs, which may be either premixed or separate, one or more uniquely labeled dNTPs and/or rNTPs, such as biotinylated or Cy3 or Cy5 tagged dNTPs, or other post synthesis labeling reagent, such as chemically active derivatives of fluorescent dyes, enzymes, such as reverse transcriptases, DNA polymerases, and the like, various buffer mediums, e.g. hybridization and washing buffers, prefabricated probe arrays, labeled probe purification reagents and components, like spin columns, etc., signal generation and detection reagents, e.g. streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

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The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

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Example 1 - Generation of human cDNA array

686 cDNA fragments corresponding 686 different human genes were amplified from quick-clone cDNA (CLONTECH) in 686 separate test tubes using a combination of sense and antisense gene-specific primers: (Set No. 9, described *supra*). Amplification was conducted in a 100-μl volume containing 2 μl of mixture of 10 Quick-clone cDNA from placenta, brain, liver, lung, leukocytes, spleen, skeletal muscle, testis, kidney and ovary (CLONTECH), 40 mM Tricine-KOH (pH 9.2 at 22°C), 3.5 mM Mg(OAc)₂, 10 mM KOAc,

75 µg/ml BSA, 200 µM of each dATP, dGTP, dCTP and dTTP, 0.2 µM of each sense and antisense gene-specific primers and 2 µl of KlenTaq Polymerase mix. Temperature parameters of the PCR reactions were as follows: 1 min at 95°C followed by 20-35 cycles of 95°C for 15 sec and 68°C for 2 min; followed by a 10-min final extension at 68°C. PCR products were examined on 1.2% agarose/EtBr gels in 1x TBE buffer. As a DNA size marker a 1 Kb DNA Ladder was used. ds cDNA was then precipitated by addition of a half volume of 4M ammonium acetate (about 35 µl) and 3.7 volumes of 95% ethanol (about 260 μl). After vortexing, the tube was immediately centrifuged at 14,000 r.p.m. in a microcentrifuge for 20 min. The pellet was washed with 80% ethanol without vortexing, centrifuged as above for 10 min, air dried, and dissolved in 10 µl of deionized water. Yield of ds cDNA after the amplification step was about 5 µg. The ds cDNA fragments for all 686 genes were cloned into TA-cloning vector using the manufacturer's recommendations (Invitrogen) and identity of the clones was confirmed by sequence analysis. The ds cDNA inserts with the sequence corresponding 686 genes were amplified by PCR using a combination of antisense and sense gene-specific primers, as described above. The ds cDNA was denatured by adding 1 µl of 10X denaturing solution (1 M NaOH, 10 mM EDTA) and incubating at 65°C for 20 min. All cDNA probes were transferred in 384-well plate and loaded on positively charged nylon membrane (Schleher & Schull) using 384 pin tool and Biomek 2000 (Beckman) robot. The resultant array is described in Table 1.

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Example 2 - Generation of ³²P-labeled oligonucleotides during first strand cDNA synthesis

Step A. cDNA synthesis/Labeling Procedure

1 μg of polyA+RNA or total RNA was converted into ³²P-labeled first-strand cDNA as follows. A sufficient volume of master mix for all labeling reactions and 1 extra reaction was prepared as follows to ensure sufficient volume. For each 10-μl labeling reaction, the following reagents were mixed:

- 2 μl 5X First-strand buffer (250 μM Tris-HCl pH8.3; 375 mM KCl; 15 mM MgCl₂)
- 1 μl 10XdNTP mix (500 μM dGTP, 500 μM dCTP, 500 μM dTTP, 5 μM dATP)
- $4 \mu l$ [α 32 P]dATP (Amersham, 3000 Ci/mmol, 10 mCi/ml)
- 1 μl MMLV reverse transcriptase (Amersham, 200 units/μl)

8 μl Final volume

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Next, the following reagents were combined in a 0.5-ml PCR test tube:

1 μg (1-2 μl) polyA+RNA sample

1 μl 10x gene-specific primers mix (0.2 μM of each oligonucleotide ID No.

2,4,6,8,10,12,.... 1372 from Table 1 of U.S. Patent Application Serial No.

08/859,998, the discosure of which is herein incorporated by reference.)

10 As a control, in separate test tube were mixed 1 μg of polyA+RNA sample with 1 μl of oligo dT primer (CDS1, 5'-d(TCTAGAATTCAGCGGCCGC(T)₃₀VN) - 3'

(where V=G or A or C; N=G or A or T or C)

For each tube, ddH₂0 was added to a final volume of 3 μl and the contents were mixed and spun briefly in a microcentrifuge. The tubes were then incubated in a preheated PCR thermocycler at 70°C for 2 min. The temperature in thermocycle was reduced down to 50°C and the tube contents were incubated for 2 min. 8 μl of master mix as prepared above were added to each reaction test tube. The contents of the test tubes were then mixed by gentle pipetting. The tubes were then incubated in a PCR thermocycler for 20 min at 50°C.

The reaction was then stopped by adding 1 μl of 10X termination mix (0.1 M EDTA, 1 mg/ml glycogen).

Step B. Column Chromatography

The 32 P-labeled cDNAs were separated from unincorporated 32 P-labeled nucleotides and small (<0.1- kb) cDNA fragments using the following procedure for each test tube. A CHROMA SPIN-200 column (CLONTECH, Palo Alto, CA) was placed into a 1.5-ml microcentrifuge tube, the water was allowed to drain through the column by gravity flow until the surface of the gel beads emerged in the column matrix. The sample was then applied to the center of the gel bed's flat surface and allowed to be fully absorbed into the resin bed. 25 μ l of ddH₂O were then applied and allowed to completely drain out of the column. 200 μ l of ddH₂O were then applied and allowed to completely drain out of the column until there was no liquid left above the resin bed. The column was then transferred to a clean 1.5-ml microcentrifuge tube.

To collect the first fraction, $100~\mu l$ of ddH_2O were added to the column and allowed to completely drain out of the column. The second, third and fourth fractions were collected in analogous fashion. The tubes with fractions 1-4 were then placed in scintillation counter empty vials, and Cherenkov counts for each fraction were obtained in the tritium channel. The fractions which showed the highest Cerenkov counts were pooled.

Example 3 - Generation of Cy3-labeled hybridization polynucleotide target from polyA+RNA using postsynthesis labelling procedure

In this procedure for generating labeled cDNA target, polyA+RNA is first converted 10 into cDNA that has primary amino groups which are subsequently coupled with Cy3 succinimide ester. This technology allows for a significant increase (about 10 fold) in activity of labeled polynucleotide target and therefore increases the overall sensitivity of detection of gene expression. The same procedure can be used for labeling two (or more) samples of RNA. In this case the cDNA synthesis step was the same for both samples but at 15 the labeling step, each cDNA sample was labeled by different and distinguishable labels, e.g. Cy3 and Cy5, Alexa 532 and Bodipy TR, Fluorescein and tetramethyl rhodamine, etc. Each labeled probe was purified separately by column chromatography and, after normalization, were combined together in equal ratio and hybridized with a cDNA array. After hybridization, the detection procedure revealed both dye-labeled hybridized target 20 simultaneously, based on the different spectral characteristics (emission wavelength) of the fluorescent labels.

A. cDNA synthesis

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The 10- μ l reaction described below converted 1 μ g of polyA+RNA into aminomodified first-strand cDNA.

For each cDNA synthesis reaction:

1. Enough master mix for all labeling reactions and 1 extra reaction was prepared to ensure sufficient volume.

For each $10-\mu l$ labeling reaction, the following reagents were mixed:

- 2 μ l 5X First-strand buffer (250 μ M Tris-HC1 pH8.3; 375 mM KC1; 15 mM MgC12)
- 1 μ l 10XdNTP mix (500 μ M dGTP, 500 μ M dCTP, 500 μ M dATP, 100 μ M dTTP,

and 100 μ M allylamino dUTP)

- 1 μ l [α -12 P]dATP (Amersham, 3000 Ci/mmol, 10 mCi/ml)
- $3 \mu I H_2C$

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1 μl MMLV reverse transcriptase (Amersham, 200 units/ul)

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8 µl Final volume

2. The following was combined in a 0.5-ml PCR test tube:

 $l \mu g (1-2 \mu l)$ polyA+RNA sample

1 μ l 10x gene-specific primers mix (0.2 uM of each oligonucleotide ID No.

2,4,6,8,10,12,...... 1372) (from Table 1 of U.S. Patent Application No.

08/859,998, the disclosure of which is herein incorporated by reference.)

As a control in separate test tube 1 μ g of polyA+RNA sample was mixed with 1 μ l of oligo dT primer (SEQ ID NO. 1373 from Table 1 of U.S. Application No. 08/859,998).

- 3. ddH_2O was added to a final volume of 3 μ l.
- 4. The contents were mixed and the tubes were spun briefly in a microcentrifuge.
- 5. The tubes were incubated in preheated PCR thermocycler at 70°C for 2 min.
- 20 6. The temperature in the thermocycle was reduced down to 50°C and incubate for 2 min.
 - 7. $8 \mu l$ of master mix were added to each reaction test tube.
 - 8. The contents of the test tubes were mixed by gentle pipeting.
 - 9. The tubes were incubated in a PCR thermocycler for 30 min at 50°C.
- 25 10. The reaction was stopped by increasing temperature up to 70°C for 5 min, then cooled to 37°C.
 - 11. 1 μ l of RNase H (10 units/ μ l) was added and the tubes were incubated at 37°C for 15 min.
 - 12. The reaction was stopped by adding 40 μ l of termination mix (0.3 M sodium acetate, pH 5.0, 1 mMEDTA).
 - 13. An equal volume (50 μ l) of phenol/chlorophorm/isoamyl alcohol mix (1: 1: 1/24 v/v) was added and extraction was performed. Phases were separated by centrifugation at 14,000 rpm for 10 min.

14. Upper water phase was collected and cDNA was precipitated by adding 2.5 volumes (about 120 μ l) of ethanol.

- 15. The precipitate was collected by centrifugation at 14,000 rpm for 10 min, the supernatant removed and the precipitate was washed with 80% ethanol.
- 5 16. The precipitate was air dried and dissolved in 10 μ l of 0. 1 M sodium bicarbonate buffer, pH 9.0.

Step B. Post synthesis labeling procedure.

- 1. 1 mg of Cy3 succinimide ester was dissolved in 10 μ l of dimethyl sulfoxide and 10 μ l of amino-modified cDNA generated at step 16 was added to it.
- 2. The mixture was incubated at room temperature overnight.

Step C. Column Chromatography

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To purify the Cy3-labeled cDNAs from the unconjugated label, the following was performed for each test tube:

- 1. CHROMA SPIN-200 column (CLONTECH) was removed from refrigerator and allowed to warm at room temperature for about 1 hour. The column was inverted several times to completely resuspend the gel matrix. (Note: Check for air bubbles in the column matrix. If bubbles are visible, resuspend the matrix in the in the column buffer (ddH₂0) by inverting the column again).
- 2. The bottom cap from the column was removed, and then the top cap was slowly removed.
- 3. The column was placed into a 1.5-ml microcentrifuge tube.
- 4. The water was allowed to drain through the column by gravity flow until the surfaces of the gel beads in the column matrix were visible. (The top of the column matrix should be at the 0.75-ml mark on the wall of the column. If the column contains much less matrix, adjust the volume of the matrix to 0.75ml mark using matrix from another column.)
 - 5. The collected water was discarded.
- The sample was applied to the center of the gel bed's flat surface and allowed to be fully absorbed into the resin bed. Care was taken not allow any sample to flow along the inner wall of the column.

- 7. $25 \mu l$ of ddH₂0 were applied and allowed to completely drain out of the column.
- 8. Apply 200 μ l of ddH₂0 and allow the buffer to completely drain out of the column until there was no liquid left above the resin bed.
- 9. The column was transferred to a clean 1.5-ml microcentrifuge tube.
- 5 10. $100 \mu l$ of ddH₂0 were added to the column and allowed to completely drain out of the column.
 - 11. The second, third and fourth fractions were collected by repeating steps 9-10.
 - 12. Cherenkov counts were obtained for each fraction by counting the entire sample in the tritium channel.
- 10 13. The fractions (usually fractions 2-3) which showed highest Cerenkov counts were pooled. Waste column and the fractions (usually fraction 1 and 4) which showed less than 10% counts from peak fractions.

Example 4 - Hybridization ³²P-labeled cDNA Target with cDNA Array

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A solution of ExpressHybTM (CLONTECH) and sheared salmon testes DNA (Sigma) was prepared by prewarming 15 ml of ExpressHybTM at 50-60°C, heating 1.5 mg of sheared salmon testes DNA at 95-100°C for 5 min followed by chilling quickly on ice, and combining the resultant heat-denatured sheared salmon testes DNA with the prewarmed ExpressHybTM.

A cDNA Array as produced in Example 1 above was then placed in a hybridization bottle and 10 ml of the solution prepared above was added to the bottle. Prehybridization was performed for 30 min with continuous agitation at 72 °C. Labeled cDNA probe (Example 1, about 200 ul, total about 2-5x10⁶ cpm) with 1/10th of the total volume (about 22 ul) of 10x denaturing solution (1 M NaOH, 10 mM EDTA) was mixed and incubated at 65 °C for 20 min. 5 μl (1 μg/ul) of human Cot-1 DNA was then added, and an equal volume (about 225 μl) of 2x Neutralizing solution (1M NaHPO4, pH 7.0) was added and incubation continued at 65 °C for 10 min. The mixtures were then combined and thoroughly mixed.

The prehybridization solution was replaced with the solution comprising the labeled oligonucleotide as prepared above and allowed to hybridize overnight with continuous agitation at 65 °C. Following hybridization, the hybridization solution was carefully removed

and discarded, replaced with 200 ml of Wash Solution 1 (2X SSC, 1% SDS). The array was washed for 20 min with continuous agitation at 65°C. Washing was repeated four times.

Two additional 20-min washes were then performed in 200 ml of prewarmed Wash Solution 2 (0.1X SSC, 0.5% SDS) with continuous agitation at 65°C. Using forceps, the cDNA array was removed from the container and excess wash solution was removed by shaking.

The damp membrane was immediately wrapped in plastic wrap, mounted on Whatman paper (3mm Chr) and exposed to x-ray film at -70°C with an intensifying screen.

Example 5 - Comparison Between Using Sets of Gene Specific Primers and oligo dT

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³²P-labeled cDNA target were synthesized by M-MLV reverse transcriptase from a mixture 588 antisense gene-specific primers (B) or oligo dT(A) using placenta polyA+RNA as a template as described in Example 2. Primer extension products generated by reverse transcription were purified by gel filtration as described in Example 2 and hybridized separately with two cDNA arrays comprising 588 human genes under identical conditions as described in Example 4. Signals which can be detected by using cDNA target generated using the set of gene specific primers but can not be detected by using conventional target generated with oligo dT primers were observed. Note, the level of non-specific background detected as signal generated by membrane alone outside of the regions with immobilized probes generated by target generated using oligo dT primers was significantly higher in comparison with the background generated by the target generated by using the sets of gene specific primers.

25 Example 6 - Generation of cDNA array probe immobilized on glass slides.

50 cDNA fragments corresponding to 50 different human genes were amplified from plasmid clones containing corresponding cDNA fragments in 96 well plates using combination of vector primer ID No. 1376 and ID No. 1377 or sense and antisense genespecific primers: ID No. 1+2, 3+4,5+6,7+8,.... 100+101 (from Table 1 of U.S. Patent Application No. 08/859,998, the disclosure of which is herein incorporated by reference). Amplification was conducted in a 400-μl volume containing 2 ng of plasmid DNA, 40 mM Tricine-KOH (pH 9.2 at 22°C), 3.5 mM Mg(OAc)₂, 10 MM KOAc, 75 μg/ml BSA, 200 μM

of each dATP, dGTP, dCTP and dTTP, 0.2 μ M of each primers and 2 μ l of KlenTaq Polymerase mix (CLONTECH). Temperature parameters of the PCR reactions were as follows: 1 min at 95°C followed by 30 cycles of 95°C for 15 sec and 68°C for 2 min; followed by a 10-min final extension at 68°C. PCR products were examined on 1.2% agarose/EtBr gels in 1 x TBE buffer. As a DNA size marker, a 1 Kb DNA Ladder was used. ds cDNA was then precipitated by addition of a 10% volume of 3M sodium acetate (pH 5-0) (about 40 µl) and 2.5 volumes of 96% ethanol (about 1 ml). After vortexing, the tube was immediately centrifuged at 14,000 r.p.m. in a microcentrifuge for 20 min. The pellet was washed with 80% ethanol without vortexing, centrifuged as above for 10 min, air dried, and dissolved in 10 μ l of deionized water. Yield of ds cDNA after amplification step was about 20 μ g. The ds cDNA was solved in 10 μ l of distilled water, 10 μ l of 1 M sodium carbonate buffer, pH 9.5, was added and the ds cDNA was denaturated by heating at 94°C for 5 min and cooled down. The treated glass slides were prepared as following: Glass slides were cleaned overnight in 25% solution of nitric acid at room temperature, washed 3 times by acetone, treated with 1% aminopropyl-trimethoxysilane for 3 hrs at room temperature, washed two times with acetone, heated at 120°C for 6 hrs and then treated with 0.2 % of para-phenylendiisothiocyanate (95:5 acetone-water solution) at room temperature for 3 hrs, then washed two times by acetone and dried in vacuum with desiccant. All cDNA probes were transferred in 384-well plate and printed on treated glass slides using 384 pin tool and Biomek 2000 (Beckman) robot. After printing, the arrays were incubated in wet chamber at 37°C overnight, then ultraviolet-cross linked to the surface by subjecting the slides to 30 mJ of energy (Stratagene Stratalinker). The arrays were washed with 1% of sodium borohydrate in 0.1 M NaOH, then washed 3 times in distilled water, dried in vacuum and stored with desiccant.

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Example 7- Hybridization Cy3 -labeled cDNA Target (or Cy3/Cy5 labeled cDNA targets) with glass cDNA array

- 1. A solution of ExpressHyb (CLONTECH) and sheared salmon testes DNA (Sigma) was prepared as follows:
 - a. 5 ml of ExpressHybTM was prewarmed at 50-60°C.

b. 0.5 mg of the sheared salmon testes DNA was heated at 95-100 °C for 5 min, and then chilled quickly on ice.

- c. Heat-denatured sheared salmon testes DNA was mixed with prewarmed ExpressHyb.
- 5 2. The glass cDNA array was placed in a hybridization container, and 1 ml of the solution prepared in step 1 above was added.

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- 3. Prehybridization was conducted for 5 min with continuous agitation at 65°C.
- 4. Labeled cDNA probe as prepared in example 3, step C13, above, (about 200 μ l) was mixed with 2 μ l (1 μ g/ μ l) of human Cot- I DNA , and denaturated at 99°C for 2 min.
- 5. The mixture prepared in Step 4 was added to the hybridization box from Step 3 and the two solutions were mixed together thoroughly. The container was sealed by sealing tape.
- 6. Hybridization was allowed to proceed overnight with continuous agitation at 65 °C.
- The hybridization solution was carefully removed and discarded in an appropriate container, and replaced with 10 ml of Wash Solution 1 (2X SSC, 0.1% SDS). The array was washed for 10 min with continuous agitation at 65 °C. The step was repeated two times.
 - 8. Additional 10-min washes were performed in 10 ml of Wash Solution 2 (0. 1 X SSC, 0.1% SDS) with continuous agitation at 65°C.
 - Using forceps, the cDNA array was removed from the container, briefly washed in 0.
 1XSSC and excess buffer was removed from surface by centrifugation in a Beckman CS-6R centrifuge at 2000 rpm.
- Glass arrays were scanned using a custom-built laser scanner equipped by green (Cy3 chanel) and red (Cy5 chanel) solid state laser built in UCLA. Images were scanned at a resolution of 20 μm per pixel.

It is evident from the above results and discussion that the subject invention provides a rapid, high throughput means to simply and quickly obtain a broad-scale screening of gene expression in a variety of different samples. Only simple hybridization protocols need be employed with the subject arrays, and signals can be detected using any convenient and readily available detection device. Despite their simplicity, assays conducted with the

subject arrays yield a large amount of information regarding the expression of numerous different and important genes in a particular sample at substantially the same time, and thus have use in many different types of applications, including drug discovery and characterization, disease research, and the like.

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All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. An array comprising a plurality of polynucleotide spots stably associated with the surface of a solid support, wherein a portion of said plurality of polynucleotide spots comprise a polynucleotide probe composition made up of unique polynucleotides and all of the unique polynucleotides on said array correspond to genes of a specific type.

- 2. The array according to Claim 1, wherein said polynucleotides of said array have an average length of from about 120 to 1000 nt.
- 10 3. The array according to Claims 1 or 2, wherein each of said unique polynucleotides does not cross hybridize with the polynucleotides of any other polynucleotide probe composition on the array.
- 4. The array according to Claims 1, 2 or 3, wherein said polynucleotide probe composition comprises a population of single stranded identical polynucleotides.
 - 5. The array according to Claims 1, 2 or 3, wherein said polynucleotide probe composition comprises a population of two different complementary single stranded polynucleotides.

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- 6. The array according to any of the preceding claims, wherein the density of spots on said array does not exceed about 500/cm².
- 7. The array according to any of the preceding claims, wherein the number of spots on said array ranges from about 50 to 1000.
 - 8. The array according to any of the preceding claims, wherein said array is selected from the group consisting of a human array, a mouse array, a cancer array, an apoptosis array, a human stress array, an oncogene/tumor suppressor array, a cell-cell interaction array, a cytokine and cytokine receptor array, a rat array, a blood array, a mouse stress array, and a neuroarray.

9. The array according to any of the preceding claims, wherein said solid support is flexible.

- 10. The array according to any of the preceding claims, wherein said solid support is rigid.
 - 11. The array according to any of the preceding claims, wherein said polynucleotide probes of said array are those listed in a table selected from the group consisting of: Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7 and Table 8.

12. A method of preparing an array according to any of the preceding claims, said method comprising:

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enzymatically generating said unique polynucleotides; and stably associating said enzymatically-generated, complementary, unique polynucleotides on the surface of said solid support.

- 13. A set of a representative number of distinct gene specific primers comprising gene specific primers corresponding to at least twenty distinct genes.
- 20 14. The set of gene specific primers according to Claim 13, wherein at least two of the twenty distinct genes are from different gene functional classes.
 - 15. The set of gene specific primers according to Claim 14, wherein the set comprises from 20 to 10,000 gene specific primers.
 - 16. The set of gene specific primers according to Claims 13, 14 or 15, wherein the set comprises primers capable of amplifying at least a portion of the polynucleotides present on an array according to any of Claims 1 to 11.
- 17. The set of gene specific primers according to Claim 16, wherein the set comprises primers capable of amplifying at least 20 of the polynucleotides present on an array according to any of Claims 1 to 11.

18. A method for detecting expression of a gene using a hybridization assay, said method comprising:

contacting at least one labeled target polynucleotide sample with an array according to any of Claims 1 to 11 under hybridization conditions sufficient to produce a hybridization pattern; and

detecting said hybridization pattern.

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- 19. The method according to Claim 18, wherein said method further comprises washing said array prior to said detecting step.
- 20. The method according to Claims 18 or 19, wherein said method further comprises preparing said labeled target polynucleotide sample.
- 21. The method according to Claim 20, wherein said preparation comprises:
 obtaining a sample of nucleic acids from a physiological source; and
 generating a population of labeled nucleic acids from the nucleic acids sample by
 using a set of a representative number of distinct gene specific primers according to any of
 Claims 13 to 17;

whereby said labeled target polynucleotide sample is produced.

- 22. The method according to Claims 20 or 21, wherein said preparing comprises conjugating a detectable label to a functionalized target polynucleotide.
- 23. The method according to any of Claims 18 to 22, where said method furthercomprises:

generating a second hybridization pattern; and comparing said hybridization patterns.

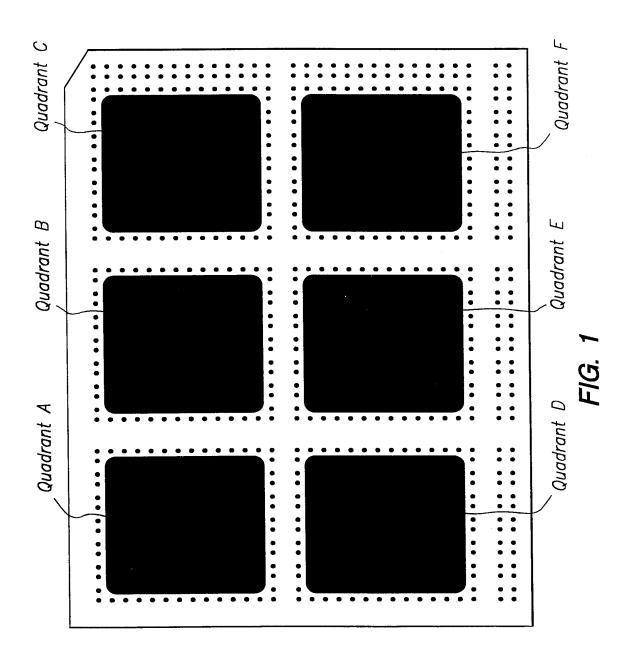
The method according to Claim 23, wherein said hybridization patterns are generatedon the same array.

25. The method according to Claim 23, wherein the second hybridization patters are generated on different arrays.

26. A kit for use in a hybridization assay, said kit comprising: an array according to any of Claims 1 to 11.

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- 27. The kit according to Claim 26, wherein said kit further comprises reagents for generating a labeled target polynucleotide sample.
- 10 28. The kit according to Claims 27, wherein said reagents comprise a set of a representational number of gene specific primers according to any of Claims 13 to 17.
 - 29. A kit for use in detecting the differential expression of genes of a plurality of physiological sources, the kit comprising:
- a set of a representative number of distinct gene specific primers according to any of Claims 13 to 17.



International application No. PCT/US98/10561

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : C12Q 1/68; C12P 19/34; C07H 21/02, 21/04 US CL :435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33, 24.5 According to International Patent Classification (IPC) or to both national classification and IPC					
B. FIELDS SEARCHED					
Minimum de	ocumentation searched (classification system followed	by classification symbols)			
U.S. : 4	435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33,	24.5			
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched					
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Extra Sheet.					
C. DOC	UMENTS CONSIDERED TO BE RELEVANT				
Category*	Citation of document, with indication, where appropriate, of the relevant passages		Relevant to claim No.		
Y	EHLERS et al. Differentiation of T cell. The in vitro acquisition of T cell. Medicine. January 1991, Vol. 173, document.	1-3, 13-15			
Y	CHALIFOUR et al. A method for a patterns. Analytical Biochemistry. 1994 see entire document.	1-3, 13-15			
Y	ZHAO et al. High-density cDNA filter for large-scale, quantitative analysis of g Vol. 156, pages 207-213, see entire do	gene expression. Gene. 1995,	1-3, 13-15		
X Further documents are listed in the continuation of Box C. See patent family annex.					
Special categories of cited documents: A* document defining the general state of the art which is not considered to be of particular relevance		"T" later document published after the int date and not in conflict with the app the principle or theory underlying th	lication but cited to understand e invention		
E earlier document published on or after the international filing date		"X" document of particular relevance; the considered novel or cannot be considered when the document is taken alone	ered to involve an inventive step		
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		"Y" document of particular relevance; th	ne claimed invention cannot be		
"O" document referring to an oral disclosure, use, exhibition or other means		considered to involve an inventive combined with one or more other such being obvious to a person skilled in	ch documents, such combination		
P document published prior to the international filing date but later than the priority date claimed		"&" document member of the same pater	nt family		
Date of the actual completion of the international search		Date of mailing of the international se	arch report		
24 JUNE 1998		7 0 AUG 1998			
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231		Authorized office JEFFREY FREDMAN Telephone No. (703) 308-0196	nce for		
Facsimile No. (703) 305-3230		1010phono 110. (703) 300-0170			

International application No.
PCT/US98/10561

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	NGUYEN et al. Differential gene expression in the murine thymus assayed by quantitative hybridization of arrayed cDNA clones. Genomics. 1995, Vol. 29, pages 207-216, see entire document.	1-3, 13-15
Y	Atlas human cDNA expression array I. Clontechniques. April 1997, pages 4-7, see entire document.	1-3, 13-15
Y	SCHENA et al. Parallel human genome analysis: Microarray-based expression monitoring of 1000 genes. Proc. Natl. Acad. Sci. October 1996, Vol. 93, pages 10614-10619, see entire document.	1-3, 13-15
Y	GOODWIN et al. Cloning of the human and murine interleukin 7 receptors: demonstration of a soluble, form and homology to a new receptor superfamily. Cell. 23 March 1990, Vol. 60, pages 941-951, see entire document.	1-3, 13-15
Y	LEONARD et al. Molecular cloning and expression of cDNAs for the human interleukin-2 receptor. Nature. 18 October 1984, Vol. 311, pages 626-631, see entire document.	1-3, 13-15
Y	GOODWIN et al. Human interleukin 7: Molecular cloning and growth factor activity on human and murine B-lineage cells. Proc. Natl. Acad. Sci. (USA). January 1989, Vol. 86, pages 302-306, see entire document.	1-3, 13-15
Y	NISHI et al. Cloning and expression of a novel variant of human interferon gamma cDNA. J. Biochem. 1985, Vol. 97, No. 1, pages 153-159, see entire document.	1-3, 13-15

International application No. PCT/US98/10561

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)			
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:			
1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:			
2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:			
3. X Claims Nos.: 4-12, 16-19 because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).			
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)			
This International Searching Authority found multiple inventions in this international application, as follows:			
Please See Extra Sheet.			
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.			
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.			
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:			
4. X No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-29, species of SEQ ID NOs: 1-10			
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.			

International application No. PCT/US98/10561

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, BIOSIS, CAPLUS

search terms: array, support, bead, nitrocellulose, nylon, filter, hybridize, anneal, DNA, RNA, gene, nucleic, oligo, polynucleotide, spot, pattern, primer

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Each of the sequences found in Tables 1-8.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons:

Each of the sequences found in Tables 1-8 represents a different nucleic acid species which are not joined by a corresponding technical feature such as encoding a similar protein.

According the Official Gazette Notice in October 1996, "Under the Unity of Invention Standard in an International Application or National Stage Application Filed Under 35 U.S.C. § 371, Up to Ten Nucleotide Sequences Will Be Searched and/or Examined Without Payment of An Additional Fee".